UNIVERSITY OF BIRMINGHAM

CONSERVATION OF CROP WILD RELATIVES' DIVERSITY IN THE FERTILE CRESCENT

By

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ABSTRACT

This thesis aims to enhance the conservation of CWR diversity in the Fertile Crescent. CWR are species of plants that are genetically close to cultivated crops. They are important sources of plant genetic materials that can be used for crop improvements. The Fertile Crescent is an important centre as it is a centre of crop domestication.

Finding CWR in the Fertile Crescent region was carried out through creating a checklist of CWR, prioritisation, collecting passport data, *ex-situ* and *in-situ* gap analysis, climate change analysis, and threat analysis.

A priority list of 220 CWR taxa was established following 12 prioritisation criteria. The priority list was revised and a new priority list consisted of 441 CWR were established. 23,878 occurrence records were collated. Ten genetic reserves are recommended.

70% of the CWR examined taxa are represented in gene banks. The most important areas for further collecting for *ex-situ* conservation are located in the west and south of Turkey. CAPFITOGEN result indicates that the top three sites with the highest CWR taxa concentration are found in eastern Turkey. The fourth highest site is found in Latakia in Syria. The result of the climate change analysis revealed that *Aegilops bicornis*, a wild relative of bread wheat, and *Triticum monococcum*, a wild relative of wheat, are expected to be highly impacted by climate change. The IUCN red assessment result indicates that out of the 88 taxa assessed, one taxon was assessed as Critically Endangered, 18 taxa as Data Deficient, three taxa as Endangered, 41 as Least Concern and 25 as Near Threatened. All these components will help the Fertile Crescent meet its targets in conserving CWR diversity as well as ensuring CWRs are preserved to prevent and tackle global food insecurity. Future work is to fill the gaps in conservation outlined in this research.

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List of abbreviations

CBD: Convention on Biological Diversity

CWR: Crop Wild Relative

ELC: Ecogeographic Land Characterization

FAOSTAT: Food and Agriculture Organization of the United Nations statistical database

GBIF: Global Biodiversity Information Facility

GIS: Geographic Information System

GP: Gene Pool

GRIN: Germplasm Resources Information Network

IPCC: Intergovernmental Panel on Climate Change

IUCN: International Union for Conservation of Nature

SDM: Species Distribution Models

TG: Taxon Group

Statement

This Ph.D. resulted in several publications and a set of papers that have been sent for publication.

Publications

1. Zair, W., Maxted, N. & Amri, A. 2017 Setting conservation priorities for crop wild relatives in the Fertile Crescent, *Genetic Resources and Crop Evolution, Springer* https://doi.org/10.1007/s10722-017-0576-3.
2. Zair, W. 2017. *Triticum monococcum*. The IUCN Red List of Threatened Species 2017: e.T172116A19398350. http://dx.doi.org/10.2305/IUCN.UK.2017-3.RLTS.T172116A19398350.en.
3. Zair, W. & Magos Brehm, J. 2017. *Triticum timopheevii*. The IUCN Red List of Threatened Species 2017: e.T71786573A71786580. http://dx.doi.org/10.2305/IUCN.UK.2017-3.RLTS.T71786573A71786580.en.
4. Zair, W. & Magos Brehm, J. 2017. *Triticum turgidum*. The IUCN Red List of Threatened Species 2017: e.T71786841A71786853. http://dx.doi.org/10.2305/IUCN.UK.2017-3.RLTS.T71786841A71786853.en. .
5. Zair, W. & Magos Brehm, J. 2017. *Triticum urartu*. The IUCN Red List of Threatened Species 2017: e.T71787307A71787310. http://dx.doi.org/10.2305/IUCN.UK.2017-3.RLTS.T71787307A71787310.en.
6. Zair, W. 2016. *Cicer bijugum*. The IUCN Red List of Threatened Species 2016: e.T98066922A98066943. http://dx.doi.org/10.2305/IUCN.UK.2016-3.RLTS.T98066922A98066943.en.
7. Zair, W. 2016. *Cicer reticulatum*. The IUCN Red List of Threatened Species 2016: e.T98067060A98067070. http://dx.doi.org/10.2305/IUCN.UK.2016-3.RLTS.T98067060A98067070.en.
8. Zair, W. 2016. *Cicer pinnatifidum*. The IUCN Red List of Threatened Species 2016: e.T98067043A98067046. http://dx.doi.org/10.2305/IUCN.UK.2016-3.RLTS.T98067043A98067046.en.

9. Rhodes, L., Bradley, I., Zair, W. & Maxted, N. 2016. *Hordeum bulbosum*. The IUCN Red List of Threatened Species 2016: e.T172092A19410413. http://dx.doi.org/10.2305/IUCN.UK.2016-3.RLTS.T172092A19410413.en.
10. Rhodes, L., Bradley, I., Zair, W. & Maxted, N. 2016. *Avena sterilis*. The IUCN Red List of Threatened Species 2016: e.T172204A19395364. http://dx.doi.org/10.2305/IUCN.UK.2016-3.RLTS.T172204A19395364.en.
11. Rhodes, L., Bradley, I., Zair, W. & Maxted, N. 2016. *Avena fatua*. The IUCN Red List of Threatened Species 2016: e.T172049A19394581. http://dx.doi.org/10.2305/IUCN.UK.2016-3.RLTS.T172049A19394581.en.

Papers sent for publications are:

CHAPTER 3: EX-SITU AND IN-SITU CONSERVATION GAP ANALYSIS OF CROP WILD RELATIVE DIVERSITY IN THE FERTILE CRESCENT OF THE MIDDLE EAST

CHAPTER 4: PROJECTED CHANGE IN DISTRIBUTION PATTERNS OF CROP WILD RELATIVES UNDER CLIMATE CHANGE: A CASE STUDY OF THE FERTILE CRESCENT

CHAPTER 5: THREAT ASSESSMENT OF CWRs

CHAPTER 1: OVERVIEW

Acknowledgment of collaborative work

Author contributions: Wathek Zair collected the data. Wathek Zair analysed the data. Wathek Zair wrote the chapter. Nigel Maxted, Ahmed Amri and Peter Winn reviewed the manuscript. Wathek Zair edited the chapter.

Wathek Zair

Date: 06.10/19

Professor Nigel Maxted

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CHAPTER 2: SETTING CONSERVATION PRIORITIES FOR CROP WILD RELATIVES IN THE FERTILE CRESCENT

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CHAPTER 3: *EX-SITU* AND *IN-SITU* CONSERVATION GAP ANALYSIS OF CROP WILD RELATIVE DIVERSITY IN THE FERTILE CRESCENT OF THE MIDDLE EAST

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CHAPTER 6: AN OVERALL SYNTHESIS TO THE THESIS

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Author contributions: Wathek Zair collected the data. Wathek Zair analysed the data. Wathek Zair wrote the chapter. Nigel Maxted, Ahmed Amri and Peter Winn reviewed the manuscript. Wathek Zair edited the chapter.

1.2. BIOLOGICAL AND AGRICULTURAL BIODIVERSITY

1.2.1. Plant diversity

Plants are not distributed equally in all regions around the world. Most of the plant diversity occurs in “megadiversity countries” (Mittermeier, 1997; 1998). Several hotspots around the world have been recognised by Myers (1988, 1990), and these have a higher number of plant species than other regions but at the same time are at great risk of deterioration. Approximately 44% of all species of vascular plants can be found in 25 hotspots containing around 1.5% of the terrestrial area of the globe (Myers *et al*, 1990). To meet the requirements of a hotspot, a region needs to comprise a minimum of 0.5% or 1500 of the Earth’s 300,000 plant species as endemics. Fifteen of the 25 hotspots comprise a minimum of 2500 endemic plant species, and ten of them comprise a minimum of 5000. The hotspots (Figure 1.1) identified include the Mediterranean Basin and the Western African Forests among others (Myers *et al*, 1990). A map that illustrates plant diversity hotspots has been created with the help of GIS tools (Figure 1.1). The map is based on Myers *et al* (1990). The idea behind displaying the hotspots on a satellite image is to distinguish between plant diversity hotspots and the green areas on the satellite image that represent the high concentration of vegetation.

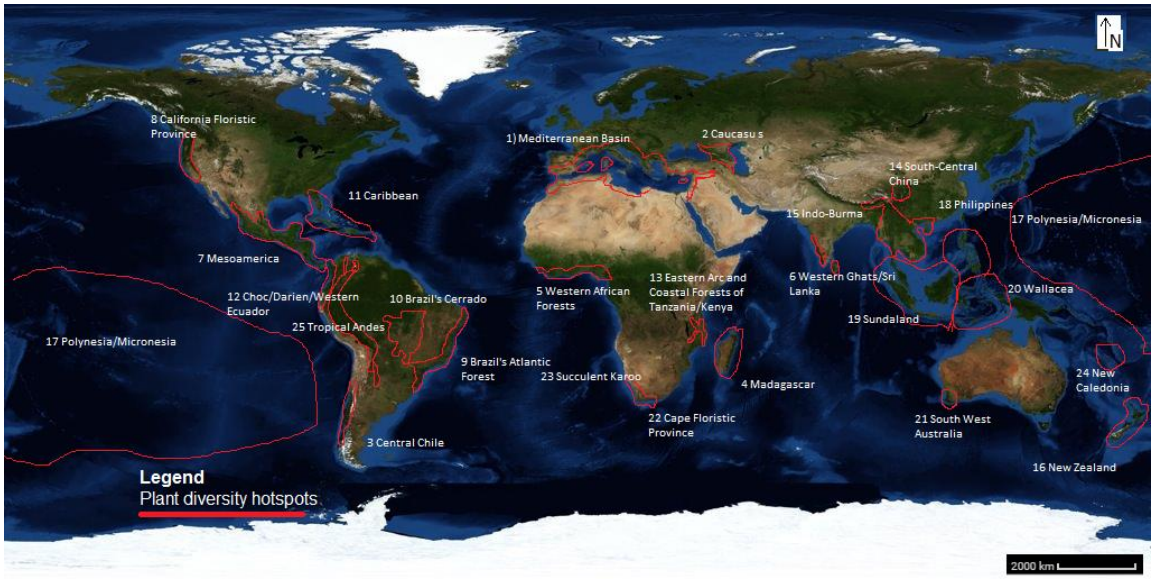

Figure 1-1. The 25 plant diversity hotspots containing a minimum of 0.5% or 1,500 of the Earth's 300,000 plant species as endemics (adapted from Myers et al, 1990).

1.2.2. The Fertile Crescent

The Fertile Crescent is part of the global hotspot "the Mediterranean Basin". As can be seen in the map (Figure 1.1), the Mediterranean Basin is a biologically diverse hotspot of global importance, primarily because of its great plant diversity. Approximately 10% of the Earth's vascular plants (25,000) exist in the Mediterranean Basin on less than 2% of the area of land on Earth, and 50% of these species exist nowhere else on the planet (Myers *et al*, 1990). The Fertile Crescent location is in Syria, Lebanon, Iraq, Jordan, Israel, Palestine, and Turkey (not the whole country in all cases) (Zohary and Hopf, 1993).

Having studied CWR in the Fertile Crescent, in my view it is vital to look at the transformation that happened from wild to domesticated crops. It is important also to look at what crops originated and domesticated in this region. Zohary and Hopf (1993) provided examples of crops that are originated in the Fertile Crescent. One of them is emmer wheat. Other examples include barley, wheat, oat, and rye. Harlan (1998) also demonstrates that the region combines the origin of several significant species such as barley, wheat, pea, lentil, and vetch that are grown in the temperate agricultural zone and date from 8,000 BC (Harlan, 1998). The wild relatives and landraces of these crops present a wide spectrum of genetic diversity (Harlan, 1998). Such a traditional agricultural system has also been dominated by various fruit-bearing trees such as almond, olive, figs, pomegranates, grapes, and pistachio, which are found in a diverse

range of weed forms, wild varieties, and locally grown varieties (Harlan, 1998). To prove a crop is domesticated and originated in an area, scientific findings must be established. Zeist and Casparie (1968) provided archaeological evidence of wild einkorn wheat from the Fertile Crescent. The seeds were taken from Mureybet in Northern Syria. Mureybet site is now under the artificial Assad Lake. The seeds were examined using radioactive carbon dating (C-14). It was suggested that the specimen dated from 7500 to 8400 B.C.

Figure 1-2. On the left are seeds of wild einkorn wheat obtained from an archaeological site in northern Syria. The seed picture on the left is taken from Zeist and Casparie (1968)

The seeds picture in Figure 1.2 has been included to compare it with recent wild einkorn wheat seeds (see image on the right) collected from Turkey by ICARDA (2008). Wild einkorn wheat's shape has undergone several changes over time.

The Fertile Crescent is an important region with high plant diversity and has major crops that are vital for human and animal food. The region also includes a variety of important medical plants as well as forage crops (Held, 1994). Nevertheless, the forest area is declining as the area is used for intensive agriculture, so desertification started and a large part of the area is a semi-desert now. Some of the land in the region is not suitable for agriculture as either it has a salty soil or it has steep slopes, which is why it needs reclamation. The ecosystems are weak; therefore, the biological diversity in the region urgently needs to be conserved and maintained (Held, 1994).

Based on the evolutionary history of many ancient human civilisations, the domestication of food crops, from a geopotential and floristic view, the Fertile Crescent is considered a region of great importance compared to other Old-World regions (Zohary, 1973; 1970). Wheat domestication started in the Fertile Crescent (Zohary, 1973; 1970). The wild relative of domesticated wheat falls to the soil when it is dry and reseeds itself. Domesticated wheat, on the other hand, remains on the spike for less

demanding reaping, and this change in wheat physiology is due to a mutation in the wild species. Wheat with this transformation was gathered more often and was used as seeds for the following season. In this way, without knowing, early agriculturists assisted this transformation in wheat physiology. The outcome is domesticated wheat, which depends on breeders to continue its life cycle (Zohary and Hopf, 2000). Early proof of the development and quality determination of crops has been left by pre-Neolithic groups in the Fertile Crescent: rye with cultivated characteristics has been discovered at Abu Hureyra in Syria from the Epipalaeolithic era (c. 11,050 BCE) (Hillman *et al*, 2001).

As crop wild relatives in the Fertile Crescent are the major focus, it is important to look at ecoregions that are found in this region. It will be important to compare CWR distribution and ecoregions as each ecoregion has different plant composition. In addition, looking at neighbouring ecoregions is important as it allows one to see how neighbouring ecoregions interact with the Fertile Crescent ecoregions and how ecoregions impact on plant distributions, especially CWR. Consequently, ecoregions of the Earth proposed by Olson *et al*. (2001) have been analysed. Olson *et al*. (2001) divided the Earth into 14 ecoregions. The Fertile Cresset belongs to the Palaearctic ecoregion. Dinerstein *et al*. (2017) divided the globe into 846 sup-ecoregions. The Fertile Crescent consists of five main subecoregions. Subecoregion one consists of a Mediterranean forest. It is alongside the coast in Syria, Lebanon, and Israel as well as south-east Turkey. This subecoregion consists of a mix of broadleaf trees and shrubs; the trees are more intense in the mountain areas. Subecoregion two consists of grassland and fewer trees with scattered shrubs. Subecoregion three consists of semi-desert area with fewer shrubs. Subecoregion four is located in the mountains of Lebanon and Syria as well as the south-west coast of Turkey. It consists of a Mediterranean forest and woodland. The tree concentration in subecoregion four is higher than other regions of a variety of broadleaf trees and shrub species. Subecoregion five consists of deciduous forests and is located in Turkey (Anatolian area).

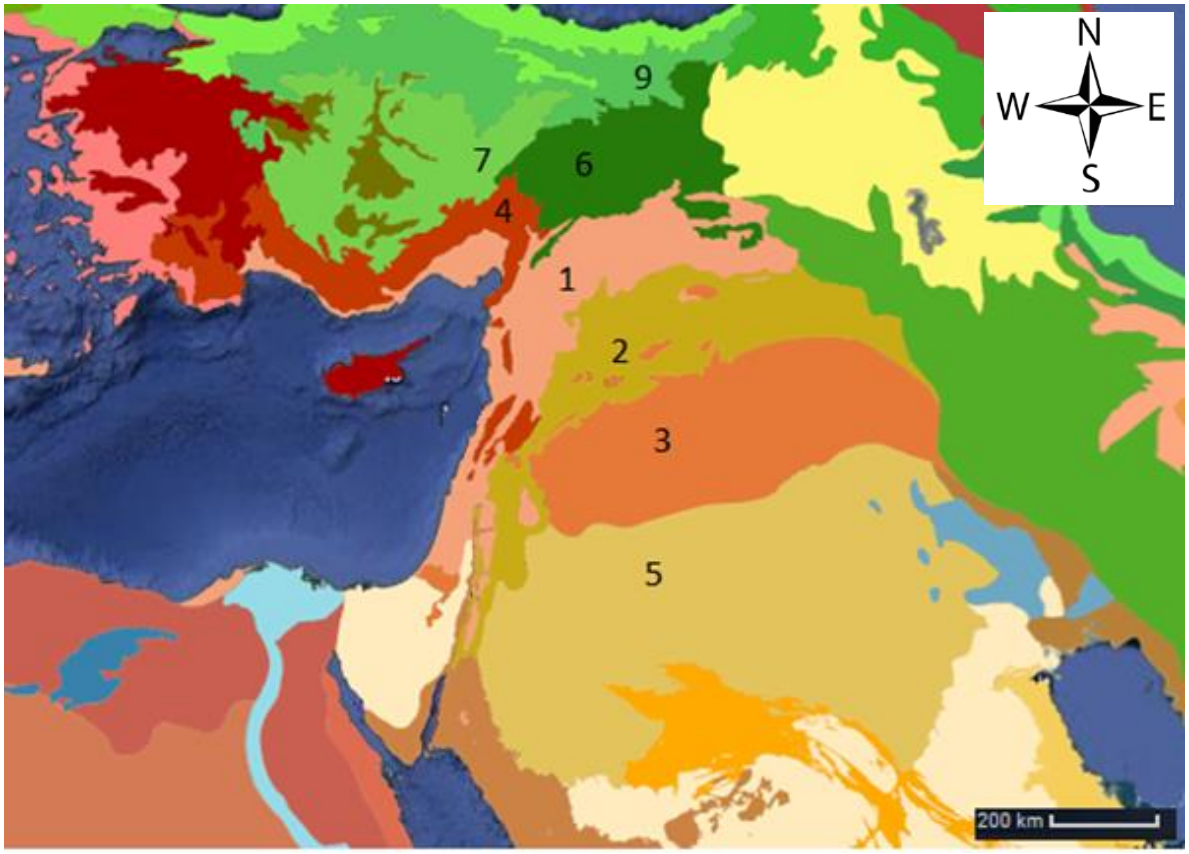

Figure 1-3. Subecoregion in the Fertile Crescent adapted from Dinerstein et al. (2017) and Resolve (2017)

As can be seen in Figure 1.3, Dinerstein *et al*. (2017) provided a broad analysis of ecoregions across the globe. However, Blondel *et al*. (2010), in their analysis of the biodiversity in the Mediterranean, looked at ecoregions around the Mediterranean Sea specifically. According to Blondel *et al*. (2010), many factors can determine the boundaries of an ecoregion; these factors can be temperature, average rainfall, as well as topography and vegetation type. One type of plant can determine a region. As can be seen in Figure 1.4, the Fertile Crescent has three subdivisions based on biogeography analysis of the region. The first subdivision is the Irano-Turanian subdivision across Iraq and Syria. The second subdivision is the East Mediterranean subdivision, across the cost area in Lebanon, Israel, Syria and Palestine. The third subdivision is the Euro-Siberian region and located in the north of Turkey. The East Sahara Arabian region plays a big part in making the Fertile Crescent drier.

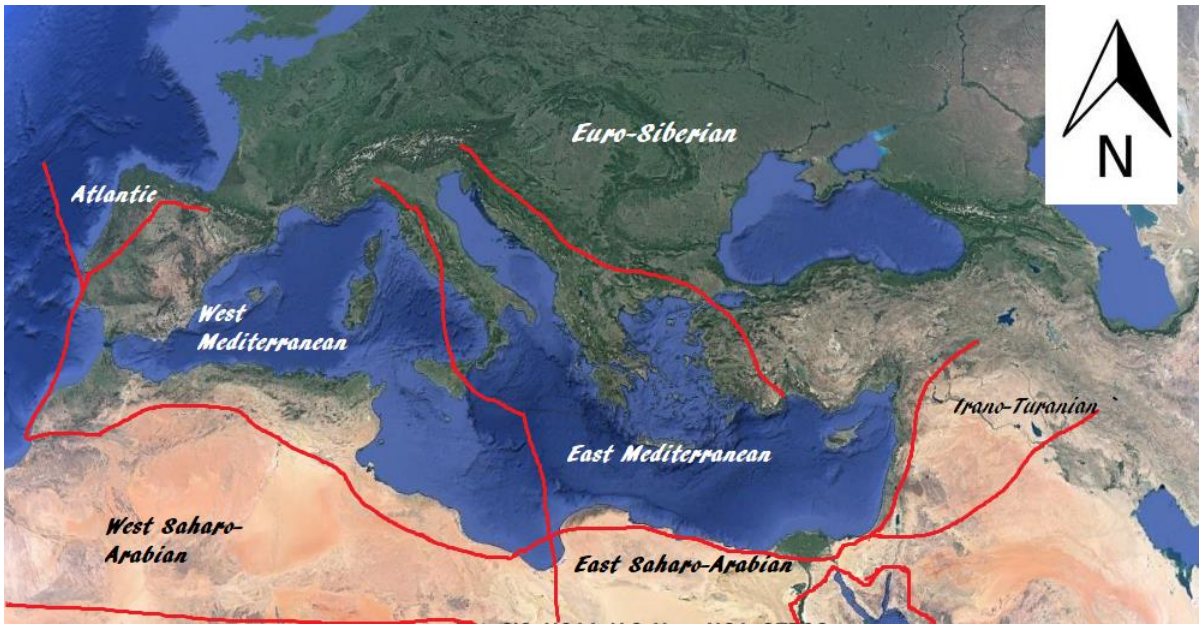

Figure 1-4. The Mediterranean region subdivision adapted from Zohary (1973) Quezel (1985) and Blondel et al. (2010).

1.2.3. Geography of the Fertile Crescent

Figure 1.5 and Figure 1.6 are maps that show the location of the Fertile Crescent.

Figure 1-5 A map showing the location of the Fertile Crescent created using ArcGIS Pro 2.4.

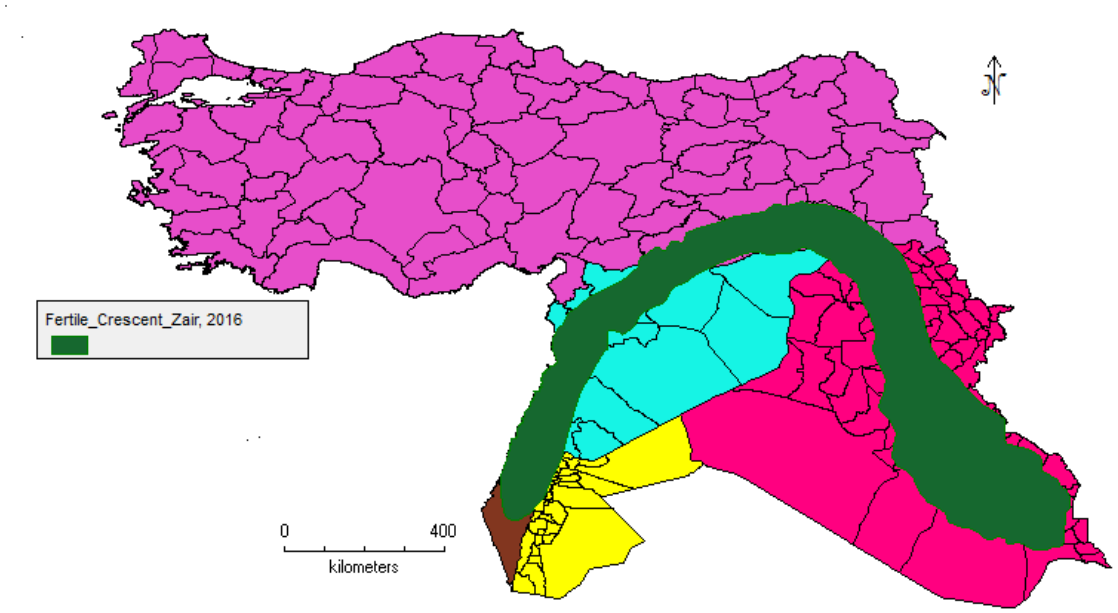

Figure 1-6. A GIS map showing the smaller size of the Fertile Crescent (Zair, 2017)

The physical geography of the Fertile Crescent is diverse as it includes upland plateaus, mountain ranges, large gravel and sandy deserts. The Fertile Crescent, as part of the Middle East region, is part of the Arabian Peninsula, which is moving away from the African plate and constitutes a part of the Anatolian Peninsula (Turkey), which seems to slide past the Asian plate (the Fertile Crescent plate map in Figure 1.7). The continental shifting has caused subduction of some of the areas below the level of the sea's surface such as the Dead Sea in Jordan. The Dead Sea is the world's deepest elevation (Goetz, 1986).

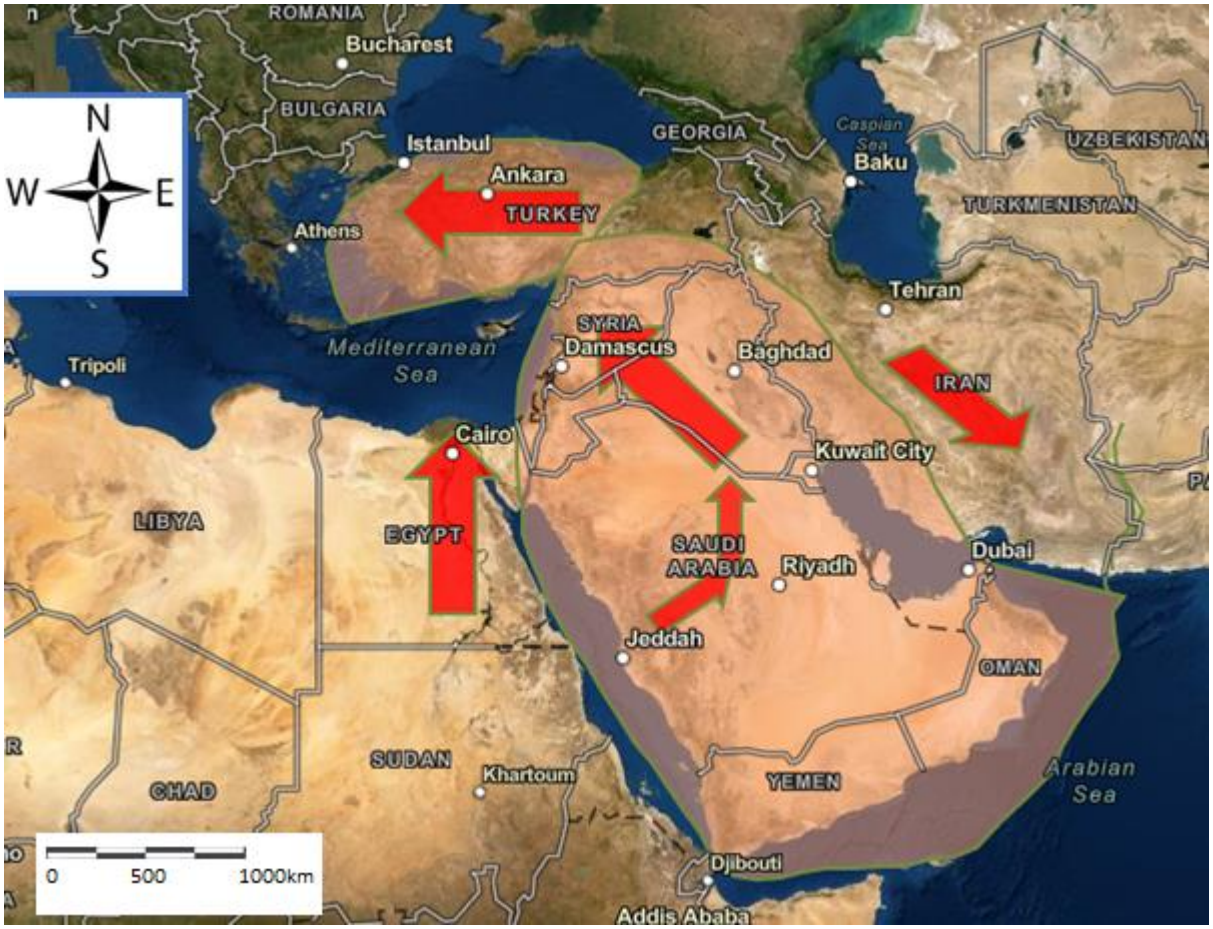

Figure 1-7. The Fertile Crescent plate map (adapted from Johnson, 1998) created using ArcGIS Pro 2.4. the red arrows represent plate movements.

1.2.4. Rivers

The Fertile Crescent region is drained by two major rivers. The first river is the Euphrates, a southwest-flowing river, which arises from the Caucasus Mountains and passes through Turkey. Euphrates subsequently turns southeast traversing across Syria and then Iraq and ends in the Arabian Gulf near Al Basra Governorate (Gibson *et al.*, 2014). The other river is the Tigris, which flows from Turkey to Syria then Iraq. Southern Iraq is the meeting point of the Euphrates with the Tigris and from there the river system continues to flow as Shatt al-Arab (Gibson *et al.*, 2014). Another important river in the region is the Jordan River, which originates from Lebanon and is considered like a border between Jordan and Israel. This river plays a critical role for the sustenance of agriculture in the region, but now it is virtually dry as its water is used for irrigation (Elmusa, 1999).

1.2.5. Mountains

Apart from the river system, the mountain chains are of biogeographical importance and hold significance in maintaining a high level of biodiversity for the Fertile Crescent. It is well recognised that these mountain chains have been hotspots for species richness. The rugged Taurus mountain chain extends from southern Turkey up to the border between Iran and Iraq. Mount Ararat is situated in the eastern part of Turkey and includes two main volcanic cones. One of the cones is the highest point in Turkey and called Greater Ararat. It is about 5,137 m above sea level. The highest peak in the entire Fertile Crescent is Mt. Damavand with an elevation of 5,670 m. Mt. Damavand is part of the Elburz mountain chain which extends over 1,000 km along the northern border of Iran with the Caspian Sea (Hickey *et al*., 1986).

1.2.6. Climate

Apart from the high mountains, most areas in the Fertile Crescent and the Arabian Peninsula region exhibit arid conditions with a scarcity of water resources (Dabour, 2006). The Middle East has hot and dry summers and not very cold winters (Al-Dabbas *et al*., 2012). The humidity, precipitation levels, and temperature fluctuate between one country and another. A heavy downpour of nearly 2,000 mm is received by the northern Caspian Sea coast in the north of Iran every year (Al-Dabbas *et al*., 2012). The desert area in the region gets considerably less or no rain for many years. The temperature gradient is also seen to vary across the Fertile Crescent. The average temperatures in the summer season are about 28–29°C and could reach 37°C. The capital city of Iraq records a very hot temperature of 49°C. In addition, Basra city recorded the hottest of 50°C among all the major Fertile Crescent cities (Al-Dabbas *et al*., 2012). Most of the storms that blow in the Middle East carry dust with them as they cross the dry desert surface. The coastal areas in the Fertile Crescent around the Mediterranean Sea, as well as Iraq and Jordan, experience a mild winter temperature. Hot summer weather prevails over the lowland desert areas in the Fertile Crescent with temperatures reaching up to 35°C or higher (Al-Dabbas *et al*., 2012).

1.2.7. Soil types

Most soil types in the Fertile Crescent are Xk- Calcic Xerosols, which accounts for around 80% of the region. A smaller portion of the region has soil type Gipsic Xerosols in some places. Yy- Gypsic Yermosols soil type can be found mostly between the

Tigris and Euphrates rivers (FAO, 2016). FAO (2016) provides the world soil map and the Fertile Crescent soil map is included (FAO, 2016). Soil type is linked to different flora.

1.2.8. History and origin of the name

A geographical term (Fertile Crescent) has been used to describe the region of Syria and Mesopotamia in ancient times, which was known as the shores of the desert bay (Clay, 1924). This term has since been broadly used in ancient history books and archaeological publications (Clay, 1924). The archaeologist Professor James H. Breasted is acknowledged as having first used the term “The Fertile Crescent”, describing it as a crescent that has a semi-circle. The open side of the semi-circle faces the south, so the centre faces the north part of the Arabian Peninsula. The west end of the semi-circle is directed toward the corner of the Mediterranean Sea in the south. The east end is directed toward the north part of the Arabian Gulf and Iran. This great semi-circle was named as the Fertile Crescent (Clay, 1924). The map Breasted created shows the name “desert bay”. The bay lies on around 400 miles of land that covers the flow of the Euphrates, and 150 miles where the Tigris flows. In 1919, Clay was interested in the history and geography of the Fertile Crescent land. In his 1919 book *The Empire of the Amorites*, Clay states that the territory was called the Amurru or the territory of the Amorites in ancient times. The country extended from the Mediterranean to Babylonia. The “desert bay” was first used by Clay (Clay, 1919). In the spring after Clay published his book, a group of explorers, known as the American Scientific Expedition, led by Breasted, followed the Euphrates River from Iraq to Aleppo. The region was also named in relation to the fertility of the land and crescent shape (Clay, 1924).

1.2.9. The birth of agriculture

This section is in this thesis because the birthplace of agriculture happened in the Fertile Crescent. As CWR in the Fertile Crescent have been studied in this thesis, it is important to look at how domestication happened in the region and how agriculture developed, to gain a better understanding of the difference between CWR and domesticated crops. There are many claims regarding where agriculture developed. Some claim that agriculture was developed in India around 3500–3000 BC (Murphy and Fuller 2016) while others claim it is in another part of the world. However,

systematic agriculture and domestication of crops started in the Fertile Crescent and humans moved from hunting and collecting seeds and vegetables from wild plants to systematic farming (Moore et al., 2000). This transformation was referred to by many scholars as the agricultural revolution. Moore et al. (2000) studied archaeobotanical samples in the Abu Hureyra site in Syria and found that rye was domesticated in the Fertile Crescent around 11000BC (Figure 1.8).

Figure 1-8. Wild rye and wheat seeds on the left were taken from the archaeological site of Abu Hureyra in Syria adopted from Moore et al. (2000) and are compared to modern rye seeds on the right, obtained from a field in Wales, UK

Moreover, Akkermans and Schwartz (2003a) indicate that agriculture started in the Fertile Crescent and archaeobotanical evidence from Tell Alaswad found that Emmer wheat was domesticated between 9000 and 8500 BC. As there is no wild emmer wheat around this site, it was concluded that this emmer wheat is a domesticated form (Akkermans and Schwartz, 2003a).

Archaeological findings from Asvan site in Turkey reinforced the theory that the Fertile Crescent was the birthplace of agriculture, as emmer wheat and hulled barley were found, and it is from the Copper Age. Moreover, free-threshing wheat was found, and it was dated from between 3300 and 2100 BC. The plant remains were extracted using water sieving among other methods. Some crop remains were also discovered and dated back to the Greek ruling period after Alexander the Great conquered the East (Nesbitt *et al*, 2017).

It is also important to look at the environmental conditions in that area around 9000 BC to have more clear evidence as crops such as wheat and barley require a certain temperature to grow. Wheat, for example, requires from 4° to 37°C for the seed to germinate (Spilde, 1989), although seed germination depends on variety and other environmental factors. It was hard to estimate how the weather was in that period since there were no weather-recording devices 10,000 years ago. Fossil pollen from

archaeological sites has been used recently to get information about the climate condition of the earth thousands of years ago, by using them as a source for radiocarbon dating (Bottema, 1995). Bottema (1995) used pollen to get information about the climate at 17 sites across the Eastern Mediterranean. As an example, the samples taken from Ghab in Syria date from 10080 BP and the summer temperature was 28^{o}C (Bottema, 1995). Such climate encourages the development and distribution of wild plants (Willcox, 2008). Before that time, between 20000 and 14500 BP, the region was covered with ice as part of the glacial period (Bar-yosef, 1998). Climate data for this period were taken from fluctuations in oxygen isotope recorded in ice and sea cores (Bar-yosef, 1998). The mountain areas near the coast in the Fertile Crescent consisted of forests in that glacial period (Bar-yosef, 1998).

Willcox (2008) illustrates that the Fertile Crescent witnessed an improvement in the climate following the Younger Dryas (Willcox, 2008). The Younger Dryas is an era of warmer climate that occurred after the end of the Post-Glacial period (Carlson, 2013). Signs from Ohalo II location suggest that humans were hunter-gatherers and their diets were based on wild plants (this site is in Israel). The wild plants were distributed across the Fertile Crescent. The evidence found consists of fossil plants derived from wild wheat and wild barley dated from 22,500 to 23,500 BP (Kislev *et al*., 1992). Humans were dependent on wild cereals as a source of carbohydrate and wild grapes and figs for their sugar content, and wild legumes for their protein. Wild olive, almond, and pistachio were used as a source of fat. There was evidence of hunting wild animals as a source of protein as animal bones have been found in the archaeological sites (Weiss, 2011). The area witnessed the domestication of sheep 11000 BP, goats 11000 BP, pigs 10500 BP, cattle 10000 BP (Zeder, 2008). Some of the evidence to prove domestication is found by using radiocarbon dating from materials in archaeological sites as well as genetic analysis (Zeder, 2008). Zeder (2008) states that the transformation from hunter-gatherer to domestication has brought an economic system, landscape change, biological diversity and an alteration in climate (Zeder, 2008). Childe (1930) suggested that the Neolithic period brought changes in lifestyle varying from domesticating crops, technology development, taming animals, religion emergence, starting to make ceramics and settlement (Childe, 1930). Cultivation can be defined as the process of growing the crop and looking after them during the

growing season (Cambridge Dictionary, 2017). The cultivation process depends on crop type and can include in the modern world tillage, seeding, irrigation, providing fertilisers, pest and disease control, weed control, and harvesting. In the past, it included turning over the soil minimally, sowing and harvesting. Domestication means bringing plants and animals under human control (Cambridge Dictionary, 2017). This definition can be expanded upon in relation to crops as the process of selecting favourite traits and collecting the seeds then planting them in a large area using engineering methods to have larger yield compared to collecting seeds from wild crops. Hunter-gatherers went into the field and chose crops that have large seeds, seeds that have been collected and replanted in other places, and by doing so, domesticating developed. Domestication in the past included settlement, as plants were domesticated by humans (Willcox, 1995). Darwinian evolution theory explains that species are established through natural selection of genetic resources so they can reproduce and survive in their natural environment (Darwin, 1859). When applying the theory to crops and domestication, it can be noted that plant species developed and the selection was done by humans (hunter-gatherers in the case of the Fertile Crescent), and that is how domestication took place. Consequently, at the present time there are varieties that exist today which are the result of thousands of years of selections and cultivations.

It was acknowledged that the transformation from gathering to farming was done gradually over a long period (Willcox, 2008). Willcox (2008) came to this conclusion after examining four sites in Syria. Three of those sites have evidence of early cultivation of cereals and fruit dated from 9000 to 10000 BC. The surprising fact is that these cereals, including einkorn wheat, rye and lentils, were cultivated away from their natural habitat. It was also noted that the climate in that time became hotter and wild species moved their sites north following their favourite climate (Willcox, 2008). Willcox (2008) suggests that domestication brought production and an economic structure.

There are many claims that settlement and domestication led to writing; however, it did not happen at the same time as domestication took place (10000 BC), and archaeological evidence suggests that writing was invented around 3100 BC in the Fertile Crescent by the people of Sumer (Fagan and Beck, 1996).

1.2.10. Consequences of domestication

After domestication started in the Fertile Crescent, agriculture was introduced to new regions such as Europe and Egypt. Irrigation systems developed as those new areas have harsher climates than the Fertile Crescent, and crops were not able to support themselves without irrigation. Some varieties adapted to the newer environmental conditions. After cereals and legume domestication, fruit trees were domesticated at around 4000 BC (Zohary and Spiegel-Roy, 1975).

Domestication let to settlements and people started living next to their gardens and building houses (Zohary and Spiegel-Roy, 1975). Population started to increase and cities started to be built. Eridu city seems to be the first city that was established. Archaeological discoveries revealed cemeteries and temples in Eridu city by using radiocarbon dating, and it was estimated that the city dated from 5400 BC (Leick, 2001).

To improve food digestibility, cooking was invented after fire was discovered (Miller, 2002). Many changes have occurred after domestication, including changes in the environment and landscape. Social changes have also been detected. Farming began with the Natufian people (Bar-yosef, 1998). The Natufian culture can be seen in the dwelling types, art items and grinding tools across the Fertile Crescent. Evidence of the economic development and social change during the Neolithic period has been detected from the archaeological remains (Bar-yosef, 1998). After domestication took place in the Fertile Crescent, food supply increased and there was surplus food to feed nobles and kings. Armies started to be established to protect food sources. Metal tools were invented. Economic changes started and the economic system was developed (Diamond 2002). Agriculture then spread to Europe and India following the migration of people. Political and social power were reallocated to Europe with the migrants (Diamond 2002).

The Fertile Crescent has been well established as an important agricultural centre across the world. The total area harvested as well as production value have been used to provide an indication of how important agriculture is in an area. Land on Earth can be classified in regard to agriculture into the following: area harvested, as land has the potential to be used for agriculture, and areas are difficult to be used in agriculture due to several factors such as urbanisation, desert or protected areas. To give more

precise evidence of the area harvested, yield and production value, meta-analysis has been utilised and a statistical analysis has been conducted that combines the results of multiple scientific studies summarised in FAOSTAT (2017). For each country in the Fertile Crescent, the area harvested has been calculated individually. The total area harvested for the whole region was then calculated by totalling the area harvested in each country. The total area harvested was 277,876.5 km^2 in the Fertile Crescent in 2014 (FAO STAT, 2017). The total area harvested amounted to 18% of the total area of the Fertile Crescent which is 1,532,480 km^2 (Turkey 783,400 km^2, Syria 185,200 km^2, Lebanon 10,450 km^2, Jordan 89,340 km^2, Israel + Palestine 26990 km^2 and Iraq 437,100 km^2). Around 137,950,751 tonnes in total were produced of all crops in 2014 in the Fertile Crescent (FAO STAT, 2017). Around 28,004,980,000 USD were generated in 2011 from major crops in the Fertile Crescent (FAO STAT, 2017).

1.2.11. Why do some places in the world get more active agriculture than others?

Weissenbacher (2009) demonstrates that environmental factors have been proven to be a major influence on emerging agriculture in one place compared to another. Some regions exhibit a high level of biodiversity compared to other regions and areas of high biodiversity favour the emergence of agriculture. Animals and plants are not distributed equally and, in some areas, vegetations and resources are scarce and, as a consequence, domestication takes place. Weissenbacher (2009) illustrates that the Fertile Crescent is the cradle of agriculture, due to its climate conditions which support agriculture and crop development. However, the notion that climate conditions support agriculture draws arguments. Some argue that due to drought and the lack of rain in recent years in the Fertile Crescent, crop production has been impacted adversely and climate change contributed to a major reduction in agriculture (Kelley *et al.*, 2015). The second factor that makes the Fertile Crescent the cradle of agriculture is its soil fertility (Weissenbacher, 2009). This is also a debatable issue since many factors have been contributing to declining soil fertility including increasing soil salinity due to drought, urbanisation, and pollution of land and water (Gunal, 2015). The third factor that makes the Fertile Crescent the cradle of agriculture is the topography of the region (Weissenbacher, 2009). The region has different elevations from the lowest point on Earth, which is the Dead Sea (Goetz, 1986), to the Greater Ararat (the highest

elevation) at 5,137 m high (Hickey *et al*., 1986). The diverse topography has been providing various environmental conditions that support a variety of crops (Weissenbacher, 2009).

Cereals and pulses are the basis of agriculture in the region and the Fertile Crescent was packed with them before domestication (Diamond, 1999). Cereals and pulses availability led to domestication. In the Mediterranean Basin, 32 out of the world's 56 species of large-seeded grass have been found to exist (Diamond, 1999). The climate in the Fertile Crescent favours the establishment of these largely seeded cereals as the region has hot summers and moderate winters. The Fertile Crescent has advantages over other regions as wheat and barley are domesticated there (Weissenbacher, 2009). The self-pollinating behaviour that wheat and barley exhibit has made it easier for the crop to be domesticated (Frankel, 1997). Other regions such as Mesoamerica where corn was domesticated have less advantages in this issue as corn is pollinated by wind, making it difficult to control as new varieties appear. Furthermore, wild wheat and barley grow in groups while corn grows individually. Farmers in the Fertile Crescent depended on water from the main rivers to water their crops. In locations that are not supplied by rivers, rain feed was employed by farmers to water crops. In 5500 BC irrigation canals started to appear and these were clearly visible in archaeological sites (Weissenbacher, 2009). Perennial irrigation was used in the Fertile Crescent and this method includes establishing canals to water the land constantly (Hill, 1997). The water moved by gravity through the canals to the farm. Another method of irrigation that was used is called basin irrigation where water is driven from rivers and then retained to realise its sediment. The evidence of basin irrigation is written in a script found in the area dated from 1700 BC (Hill, 1997). There are many pieces of evidence to suggest that farmers were very skilled, and trading developed as farming was very successful in the Fertile Crescent and farmers produced more food than they could consume (Kubesh *et al.*, 2008). Therefore, trading was initiated, and the wheel was invented to transfer produce. In a later period, extensive farming caused soil salinity and certain areas could not be used to grow crops (Kubesh *et al.*, 2008). In 2017, the Fertile Crescent provided food for 160,217,948 people across the region. Information about the population of the Fertile Crescent is obtained from combining the population of each country of the Fertile

Crescent for the year 2017 from Worldometers (2017). Not only has the region provided food for its own people, the region exports agriculture produces to several other countries. For example, Turkey exported 16 billion USD value of agriculture produce in 2013 (USDA-FAS, 2014)

1.2.12. Flora

The study of flora is considered a type of classification or taxonomy study. According to Davis and Heywood (1963), taxonomy is the science of identifying and naming species. Flora is the study of plant species that grew in a particular geographical location (Davis and Heywood, 1963). The definition does not contain plant species that are introduced for commercial use (Davis and Heywood, 1963). The study of flora can be on the national, regional or on a continent level. Each country of the Fertile Crescent has its distinctive flora. Flora is the plant composition that distinguishes one area from another. Lebanese and Syrian flora has more than 3,500 species. To have a clear idea about the type of flora in the Fertile Crescent, an example of the flora of Syria has been presented (Ibrahim *et al.*, 2015). Ghab in Syria gives an idea of how flora is classified according to elevations in the Fertile Crescent. Category one is called the hot Mediterranean floor. It is found up to 300m above sea level and consists of *Ceratonia Siliqua* (Ibrahim *et al.*, 2015). Category two is called the real Mediterranean floor. It combines plants that are found from 300 to 850 m above sea level. Examples of those species are *Quercus calliprino, Pinus prutia, Cupressus sempervirens, Phillyrea media, Olea europaea, Rhus coriaria, Rhus cotinus, Rhamnus palaestina* and *Cercis siliquastrum* (Ibrahim *et al.*, 2015). Category three is called the upper Mediterranean floor. It is located between 850 and 1200m above sea level. This category consists of deciduous trees such as *Quecrus infectoria, Pirus syriaca, Amygdalus orientalis,* and *Sorbus torminali* (Ibrahim *et al.*, 2015). Category four is called the Mediterranean mountain floor. It is located 1200m above sea level. Examples of species that are found in the Mediterranean mountain floor are *Cedrus libani, Quercus pseudo cerri, Juniperos drupacea* and *Salix alba* (Ibrahim *et al.*, 2015). The flora in the Fertile Crescent has many advantages over other regions. It contains a high level of cereals and pulses.

The Fertile Crescent has CWR related to 4 out of 12 major crops internationally as of 2014. The data to confirm the 12 major crops worldwide are taken from FAOSTAT

(2017). The crops are listed based on their production quantity in tonnes (Figure 1.9). The figure was created based on data extracted from the FAOSTAT (2017) database for each country and all crops were then listed based on the production quantity from high to low.

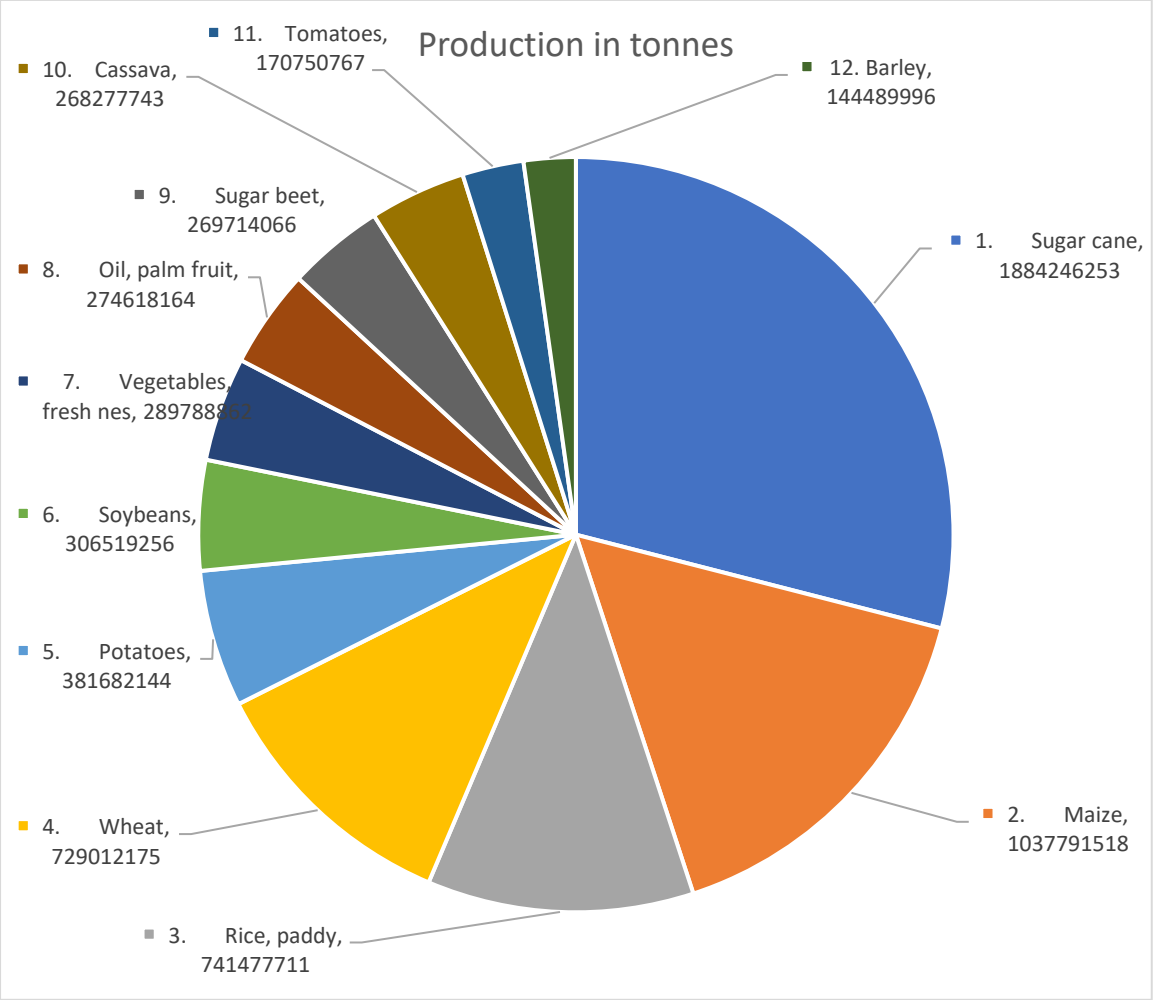

Figure 1-9. Production value of 12 major crops worldwide in 2014 based on FAOSTAT (2017) data

It was estimated that 390,900 vascular plants are known to humans (RBG Kew, 2016). The plant taxa number in the Fertile Crescent is not known. To estimate the number of taxa in the Fertile Crescent, flora that was completed for each country was looked at. The problem is that most of these floras were completed a long time ago and they need updating as there are new taxa names that have been recorded. After looking at each flora individually, a recent work done by Ghazanfar and McDaniel (2015) entitled "Floras of the Middle East" was looked at. For Syria, according to Post (1932-1933) and Ghazanfar and McDaniel (2015), the number of plant taxa is 3,500 taxa. This

number consists of naturalised species as well as native ones. For Palestine and Israel, the number of plant taxa is estimated to be 2,700 according to Ghazanfar and McDaniel (2015) and Zohary (1966–1986). Lebanon has 2,606 plant species according to Mouterde (1970) and Ghazanfar and McDaniel (2015). For Iraq, the taxa number is 3,220 according to Ghazanfar and McDaniel (2015). Jordan has over 2,600 vascular plants belonging to 122 families (Taifour and El-Oqlah, 2017). Guner *et al* (2012) provided a list of plants in Turkey consisting of 9,753 taxa. The total number of vascular plants in the Fertile Crescent was calculated based on the above-mentioned sources. The total number is 24,379 taxa. The number was then compared with the total number of taxa of the world from RBG Kew (390,900 taxa), and this number is increasing on a daily basis (RBG Kew, 2016). As can be seen in Figure 1.10, the Fertile Crescent is home to 6.23% of the plants in the world.

By looking back at Myers *et al.*'s (1990) hotspots criteria it can be seen that the Fertile Crescent is a hotspot for plant diversity as it has more than 0.5% of the Earth's plant species; however, it is not on its own as the plants need to be endemic. Not all the plants listed in the Fertile Crescent (24379 taxa) are endemic as there are naturalised species. That is why the Mediterranean Basin is a hotspot and the Fertile Crescent is part of it.

Turkey has the highest percentage of plant taxa in the Fertile Crescent and it contains 2.4% of the world's plant taxa. Syria has the second largest percentage of taxa in the Fertile Crescent and contains 0.89% of the world taxa. Iraq has the third largest vascular plant number in the Fertile Crescent. The percentage of the vascular plant in Iraq is 0.82% of the world's taxa. Palestine and Israel have 0.69% of the world's plant species. Jordan has the same as Lebanon with 0.66% of the world's plant taxa and they both have the lowest percentage of taxa in the Fertile Crescent. This analysis reflects an illustration of the number of plants in the Fertile Crescent and it is clearly concluded that Turkey has the highest number. The number of taxa was then also compared with the area of a country as Turkey is a large country 783,562 km^2 and it is important to get an idea about the taxa per unit area (taxa per 1 km^2). Calculating taxa per km^2 can be done by dividing the number of taxa in a country to the country area in km^2. A conclusion can be determined (summarised in Table 1.1 below) that Iraq has the lowest taxa per km^2, and this is actually the case as the country has a

large desert which has no plants at all in some parts. Each km^2 in Iraq has 0.007 taxa. Lebanon has the highest concentrations of taxa per kilometre square as it has 0.24 taxa/ km^2. Jordan has the second highest taxa per km^2 (0.028 taxa/ km^2). Syria has the third highest taxa per km^2 (0.018 taxa/ km^2). Turkey is in the middle at 0.012 taxa/ km^2. Palestine and Israel are the second lowest after Turkey having 0.010 taxa/ km^2. The Fertile Crescent has 6.23% of the world's vascular plant taxa. The following three major elements were then plotted together: the number of taxa in the Fertile Crescent per country, the area of each country in km^2 and taxa per km^2. The size of the ball reflects the size of the country in km^2. Syria, Iraq, Jordan, Palestine, and Israel have the same location. This means they have a similar distribution of plants per km^2 taking into account taxa number and the country area. Lebanon, which is the smallest ball to the very right, has the highest concentrations of taxa per km^2 and Turkey has the highest number of taxa.

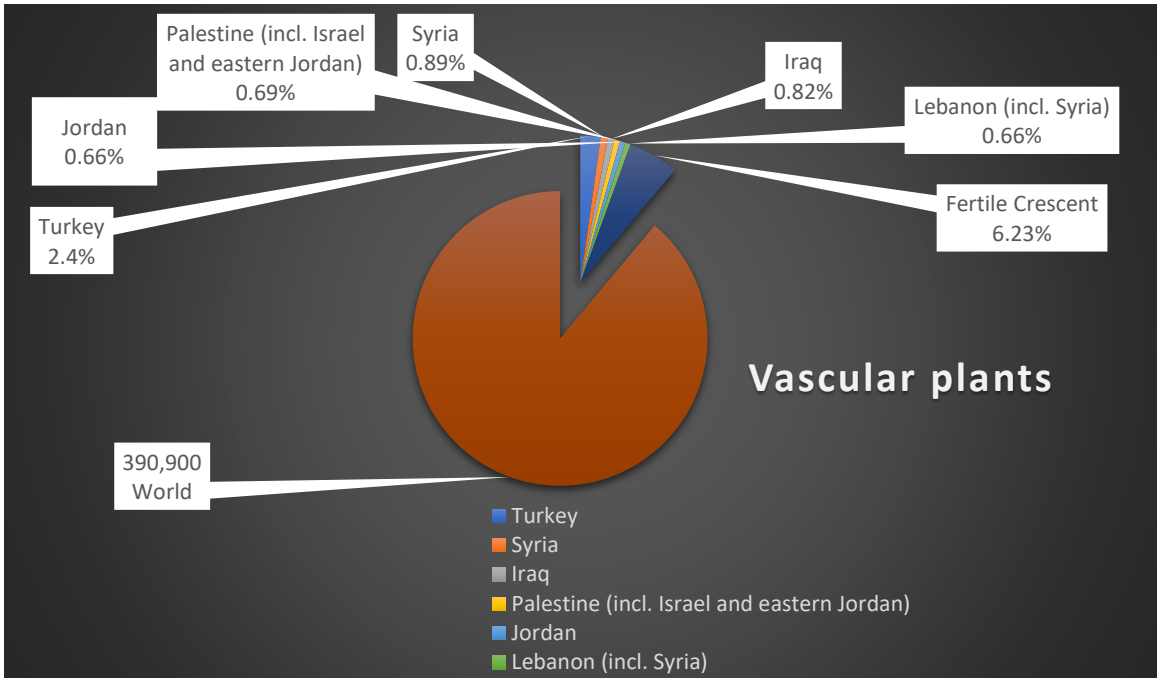

Figure 1-10. The number of vascular plants in the Fertile Crescent

Table 1.1. Taxa per km² in countries of the Fertile Crescent

COUNTRY	Country area (km²)	Taxa Per unit area (taxa/ km²)
Turkey	783,562	0.012
Syria	185,180	0.018
Iraq	437072	0.007
Palestine / Israel	26990	0.010
Jordan	89,342	0.028
Lebanon	10,452	0.24

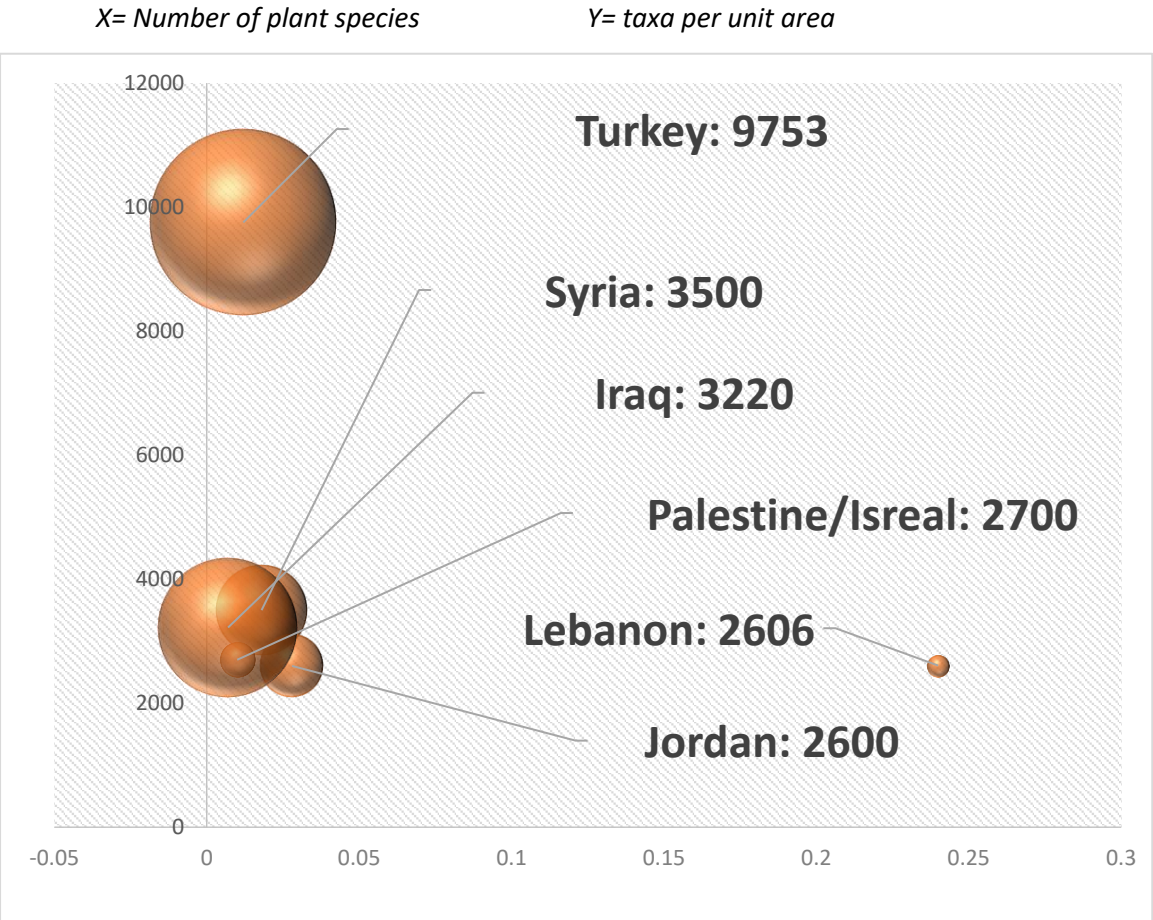

Figure 1-11. The number of vascular plants in the Fertile Crescent per country and per taxa per unit area. X reflects the number of plant species and Y reflects taxa per unit area. The size of the ball reflects the size of the country in km².

1.2.13. Native and endemic plants in the Fertile Crescent

Native plants can be defined as the plant that historically exists in a particular geographical area which were not introduced by humans or other means (CEQ, 1999). Alien plants can be defined as plants that introduce themselves to a particular location through seeds movement or rhizomes, stems or any plant materials that are able to reproduce. Invasive plants are alien plants that can cause harm to crops, humans or the environment (CEQ, 1999). Biodiversity richness can be defined as the density of plants that are endemic in an area (Caldecott, 1994). Endemism can be defined as plant species that are limited to a certain location (Decandolle, 1820). The term endemism was taken from medicine and is used to refer to an infection that is persistent in a particular village or a city (Decandolle, 1820). Turkey has the highest richness compared to other countries in the Fertile Crescent and is found in Group II. Group I is the top 25 biodiverse countries and Group II is the next ones (Nationmaster, 2017).

Taxa in the Fertile Crescent from section 1.10 Flora were then compared with endemic plant species taken from Jaradat (1998) and the result is in Table 1.2.

Table 1.2. Taxa and endemic plant species in the Fertile Crescent

Country	Taxa in the Fertile Crescent	*Endemic plant species taken from Jaradat (1998)*
Iraq	3220	190
Palestine and Israel	2,700	170
Jordan	2,600	150
Lebanon	2,606	300
Syria	3,500	400
Turkey	9,753	2,700

1.2.14. Agriculture biodiversity in the Fertile Crescent

Agriculture biodiversity can be defined as biological diversity that is relevant to agriculture and food production. It includes the varieties of plants, animal, and microorganism that are used in agriculture. The definition also includes any living organism that supports agriculture production directly or indirectly, such as pollination and beneficial insects (FAO, 1999a).

Nikolai Vavilov was a Russian scientist well known for his theory of the centre of origin for demonstrated crops. With Vavilov's theory (1926) in mind, it can be noticed that the Fertile Crescent contain two centres of origins. The first is the Asia Minor and includes a large diversity of crop gene pools (Vavilov, 1926). The second is the Mediterranean and comprises a portion of important crops (Vavilov, 1926)

Harlan (1992) states that most crops grown in the Fertile Crescent's environmental zone, either the domesticated varieties or their wild ancestral counterparts, are of worldwide importance.

1.2.15. Data on economic and social significance of crops

Information about the economic and the social significance of crops can be taken from FAOSTAT. FAOSTAT databases provide numerical values for yield for a particular crop for a specific country. The number of countries in the database is 200 and the number of crops that can be searched is 20. Users can compare yield in several countries. Data found included production (in metric tonnes), area harvested, and yield per hectare (FAOSTAT, 2016). The criteria of presenting the socio-economic value of crops contribute to establishing an action plan for conservation of CWR. In this study, the socio-economic value is represented by production in 1,000 USD, energy supply, protein supply, and fat supply.

1.2.16. Production value

Figure 1.12 shows crops with the highest economic values in the Fertile Crescent (production in 1,000 USD) for the year 2011 (FAOSTAT, 2016). The reason for choosing the year 2011 statistic is that 2011 gives a more accurate reading of the economic value of crops in the region over a long period. The reason for that is that the war that started in the region impacted heavily on agriculture especially in Syria. It is believed that this situation is temporary. For example, the production value of wheat declined from 3,858,331 thousand USD to 2,024,332 thousand USD between 2011

and 2014 in Syria (FAOSTAT, 2016). The most up-to-date statistic at the time of the study is for the year 2014.

As can be seen in Figure 1.12, the production values of tomato and wheat are the highest, amounting to 903,859 thousand USD for tomato and 3,951,780 thousand USD for wheat.

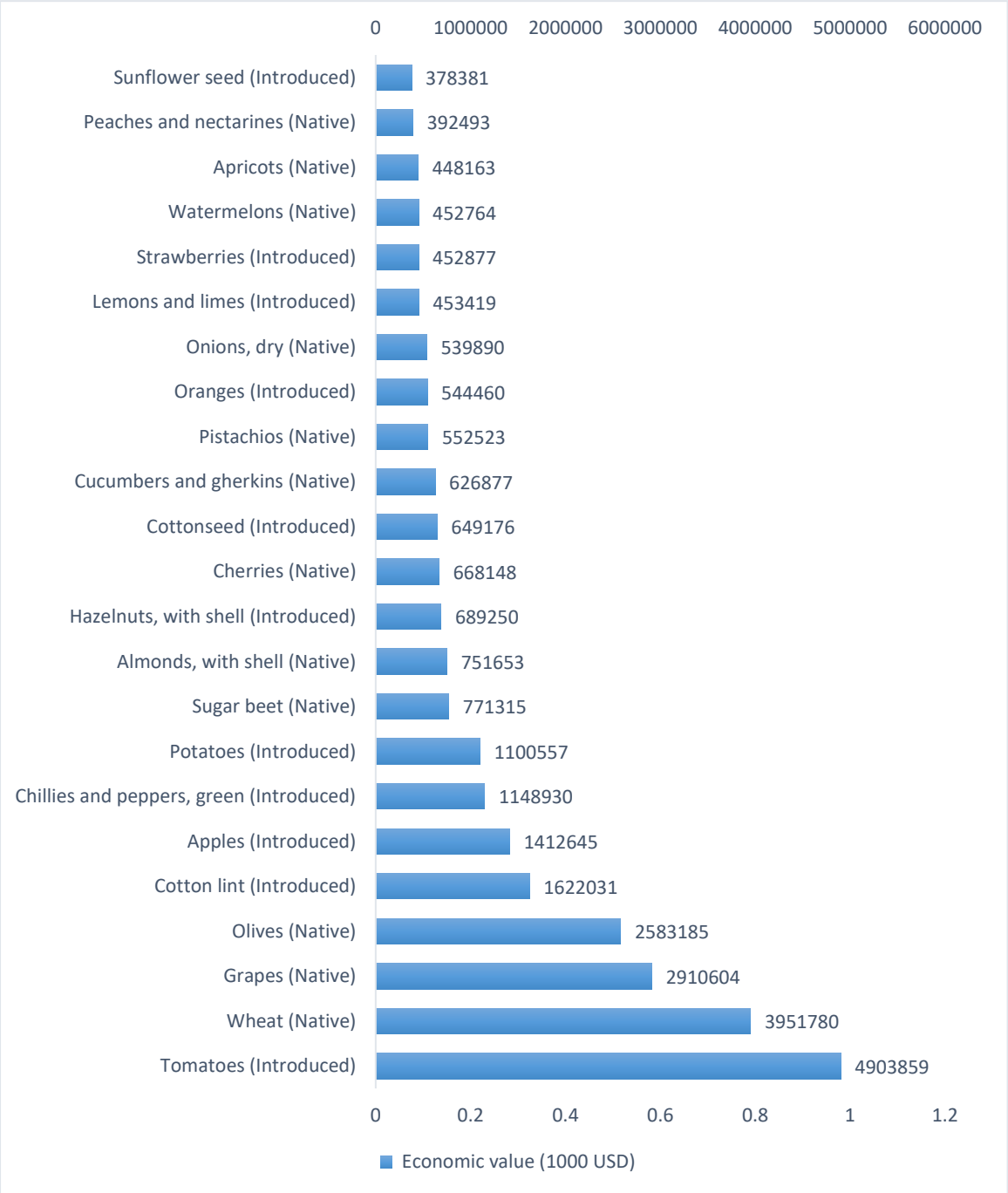

Figure 1-12. Crops with the highest economic values in the Fertile Crescent production (in 1,000 USD) in 2011 (FAOSTAT, 2016).

1.2.17. Energy supply

Energy supply from the main crops can be determined based on a diet of 2,460 kcal per capita per day. Overall, it can be seen from Figure 1.13 that people in the Fertile Crescent depend heavily on cereals which account for most the energy supply at around 42%, while maize and soybean oil account for less at around 3% each in energy supply (FAOSTAT, 2016).

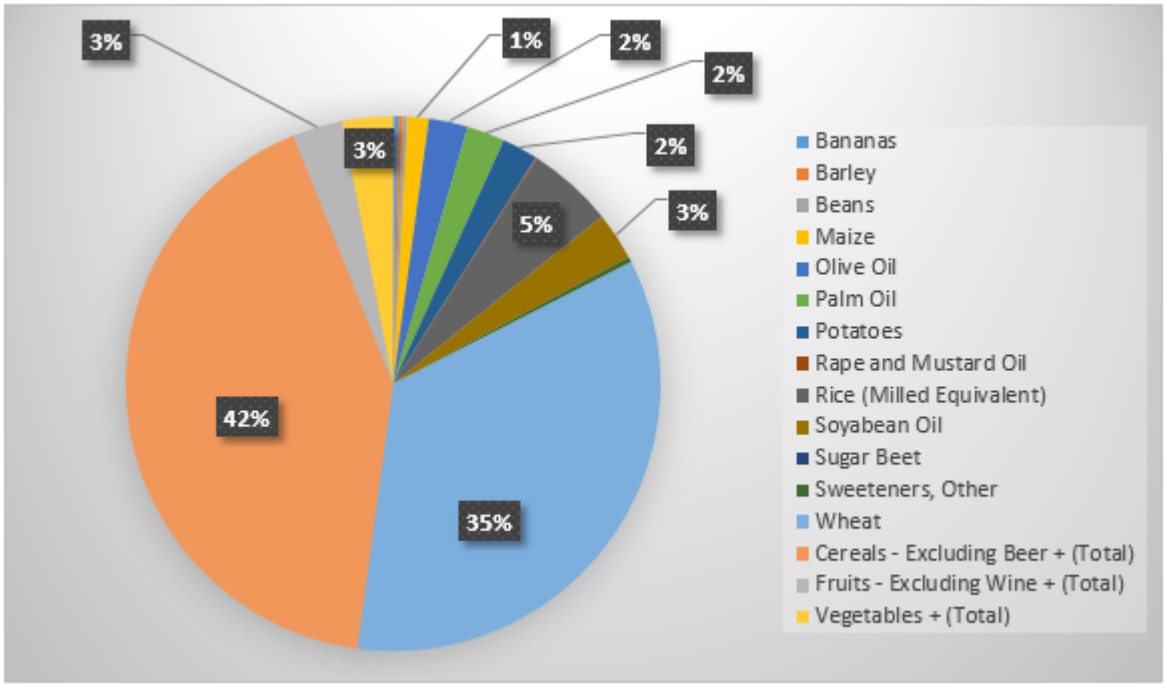

Figure 1-13. Sources of energy from the key crops consumed in the Fertile Crescent

The energy is calculated based on an average consumption of 2,460 kcal per person a day (FAOSTAT, 2016).

1.2.18. Fat supply

Fat supply from the main crops can be determined based on a diet of 2,460 kcal per capita per day as well. Overall, it can be seen from Figure 1.14 that people in the Fertile Crescent depend heavily on olive oil, palm oil, and soybean oil which accounted for most of the fat supply at around 25%, 20%, and 20% respectively, while maize and rice accounted for less (FAOSTAT, 2016).

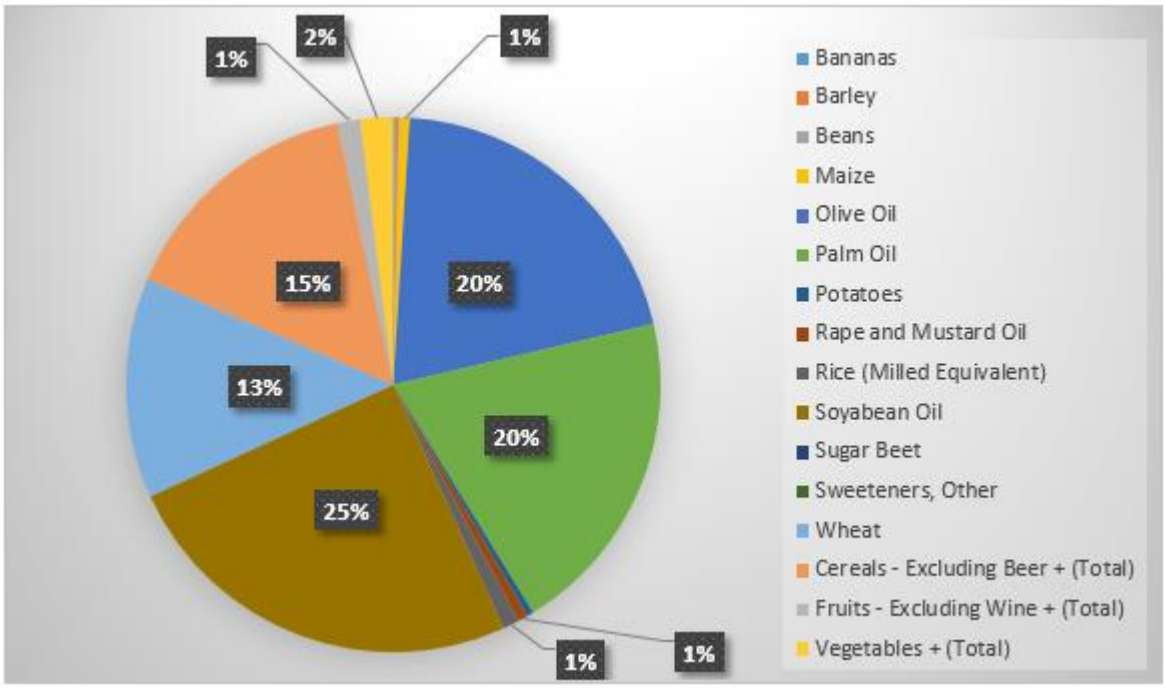

Figure 1-14. Sources of fat from the key crops in the consumed Fertile Crescent. The fat is calculated based on an average consumption of 2460 kcal per person a day (FAOSTAT, 2016)

1.2.19. Protein supply

Protein supply from the main crops can be determined based on a diet of 2,460 kcal per capita per day as well. Overall, it can be seen from Figure 1.15 that people in the Fertile Crescent depend heavily on cereals and wheat which account for most of the protein supply at around 46% and 40% respectively, while maize and rice account for less energy supply at around 1% and 4% respectively (FAOSTAT, 2016).

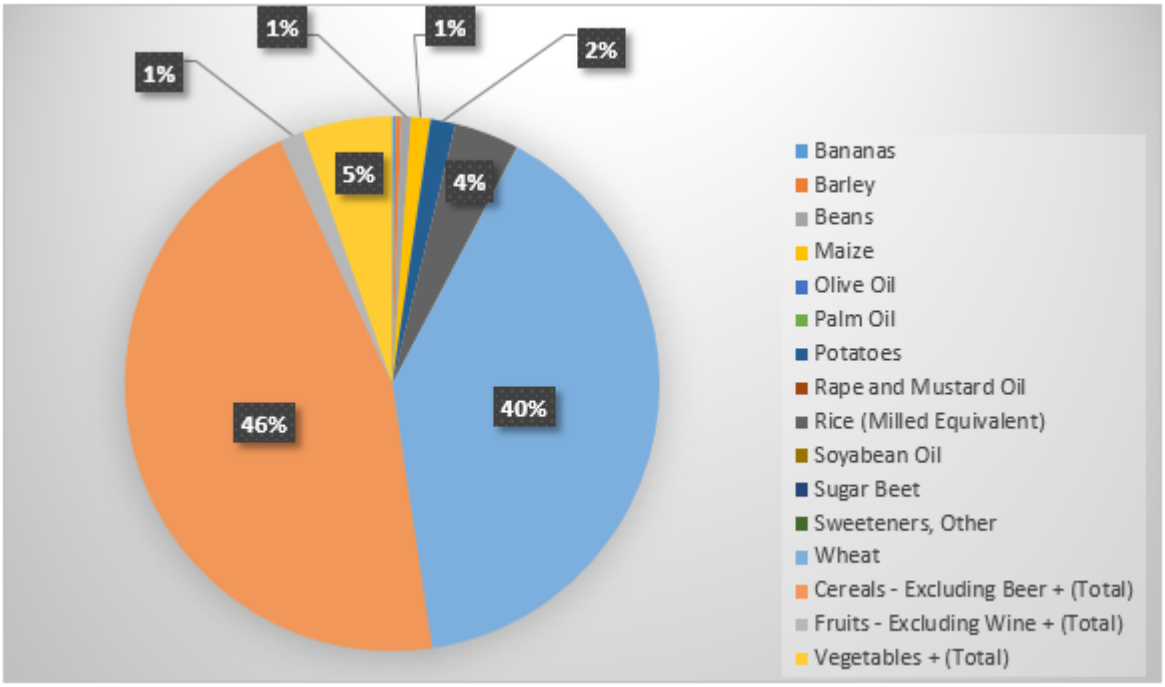

Figure 1-15. Sources of protein from the key crops consumed in the Fertile Crescent. The protein is calculated based on an average consumption of 2,460 KCal per person a day (FAOSTAT, 2016)

1.2.20. Threats to agrobiodiversity

1.2.20.1. Climate change

Human activity is the most likely major cause of climate change impacting directly on global atmospheric temperature, the temperature of the ocean, and the water cycle (IPCC, 2014). To quantify the changes in our global temperature, a sequence of observations and studies has been conducted (IPCC, 2014). It should be noted that there was a rise in the temperature of the ocean and land by 0.85°C between 1880 and 2012 (IPCC, 2014). The emission of greenhouse gases has also been growing and this has accounted for 40% more CO_2, 150% more CH4, and 20% more nitrous N2O in 2012 compared to the pre-industrial period (IPCC, 2014). CO_2 emissions from land use change and deforestation have increased in volume by 40% between 1970 and 2011 (IPCC, 2014). The prediction for the future is not optimistic. There will be a rise between 0.3°C and 1.7°C by 2100 if the world produces lower greenhouse gases, and that will increase to 4.8°C if the world produces a higher amount of greenhouse gases (IPCC, 2014).

The long-term effects of global warming include a) changes in precipitation patterns, changes in the global water cycle, snow, and ice melting and b) ecosystems change and that includes terrestrial, marine and changes in the behaviour of wildlife. Land surface temperature increase, changes in precipitation patterns, more droughts, heat waves, and desertification will influence agriculture directly (Jarvis *et al*., 2010) These changes will lead to a decrease in crop production as there will be changes in the geographical occurrence and prevalence of diseases and pests (Jarvis *et al*., 2010).

1.2.20.2. Climate change in the Fertile Crescent

The Fertile Crescent area recorded a severe drought, precipitation decrease, and a rise in temperature (Kelley *et al.*, 2015). Trigo *et al*. (2010) records showed the worst two-year drought happened between 2007 and 2009 (Trigo *et al*, 2010). As an example, in Iraq, between the year 2007 and 2008, precipitation declined to up to 70% of the average rate. The prolonged drought caused depletion of existing water and agriculture was severely influenced. This drought was the main reason behind the migration of around 1,500,000 migrants from villages and agricultural lands to big cities (Solh, 2010). There has been no record of natural disasters linked to the severe drought. Greenhouse gases are held accountable for the drought based on recent model studies (Kelley *et al.*, 2015). It has been predicted that the future is going to be hotter and drier for the area based on recent model studies (Kelley *et al.*, 2015).

The Fertile Crescent's vulnerability to drought was observed and recorded, and weather data were used to evaluate the severity of this phenomenon. In one of the climate models concerning the region, it was noted that climate change led to drought there (Kelley *et al.*, 2015). Figure 1.16 shows the Fertile Crescent's mean climate history and long-term trends (Kelley *et al.*, 2015).

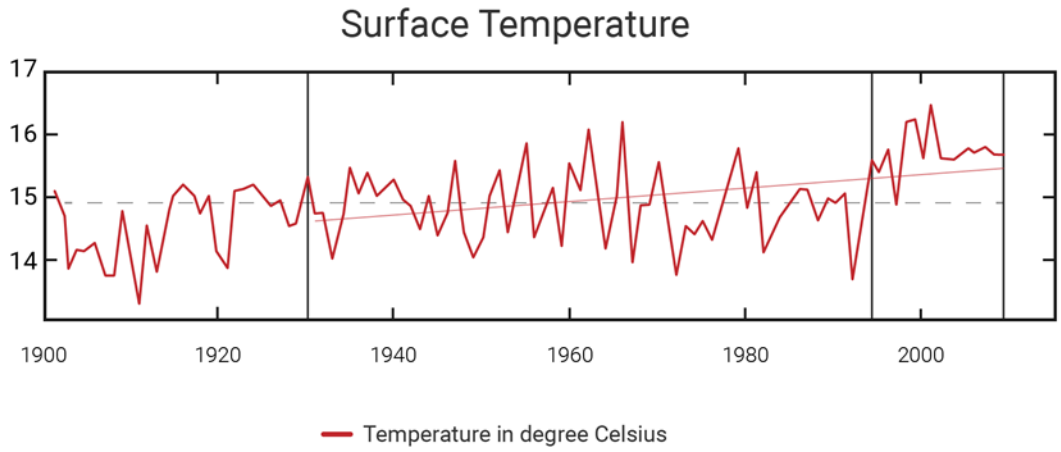

Figure 1-16. Climate change in the Fertile Crescent (annual surface temperature) based on (Kelley et al., 2015)

Trigo *et al*. (2010) state that climate change impacted negatively on vegetation in the Fertile Crescent (Trigo *et al.*, 2010). In 2008, from January to June, Normalized Difference Vegetation Index (NDVI) taken from the VEGETATION instrument found that parts of northern Iraq, eastern Syria, and south-eastern Turkey showed up to six months of stressed vegetation (Trigo *et al.*, 2010).

1.2.20.3. Statistics

Human activities and climate fluctuations have led to a degradation of 70% of the Earth's soil (Dregne and Chou, 1994). Among the total degradation, industrial and agriculture activities are the major factor for fertility loss (Lal, 1998). It is estimated that the total annual loss of 75 billion tons of soil costs the world approximately 400 billion USD a year, around 70USD / person each year (Lal, 1998). In Asia, soil erosion causes 20% of the losses of productivity in agriculture areas, especially in Israel, Jordan, Lebanon India, China, Nepal, and Pakistan (Dregne, 1992).

Threats to biodiversity are recognised on the habitats, species, and at a genetic level (CBD, 2015). Nearly 100% of natural grassland was lost in the USA since 1942 (Spellerberg, 1996). More than 90% of natural wetlands in New Zealand have been lost since the European settlement (Spellerberg, 1996). From 2000 to 2010, the annual level of forest degradation is estimated to be 13 m hectares or 130,000 km^2 per year

(FAO, 2011), falling from 16 m between 1900 and 2000. The IUCN estimates that 11,000 living organism kinds are immensely threatened with fear of extinction that consists of 70% of all species including 89 species of mammal, 129 species of bird, 21 species of reptile, and 86 species of plant. The Easter Island endemic tree, *Sophora toromiro*, is now extinct in the wild. The last specimen was chopped down and used for firewood in 1960 (Maunder *et al*., 1999). The landscape of wheat in Greece decreased from 80% in 1930 to less than 10% in 1970; recently, it is less than 1%. In Kampuchea, the unique rice varieties were lost in the 1970s. In 1949, 10,000 landraces of wheat were recorded in China. In 1970, the number of the landraces declined to 1,000 (FAO, 1998). It was recorded that 91% of apple landrace, 95% of cabbage, 94% of peas, 81% of tomato, and 91% of field maize have been lost in the United States (FAO, 1998). Lugo (1988) projected that 15–25% of the world's species would be lost by 2000. Maxted *et al*. (1997) stated that 25–35% of the vegetation and animal genetic diversity would disappear by 2000. This has turned out to be true. Humankind is increasing the rates of extinction among various species. However, extinction can also occur by natural causes. May *et al*. (1995) calculated the extinction rates by observing the typical lifespan of the species in the fossil record and habitat loss. The study found that human activities are speeding up the extinction rate. The study mentioned that, since 1600, the extinction rates have been four times higher than the background rates (May *et al.*, 1995). Rabinowitz (1981) defined the rarity based on three factors. The first factor is the geographical range. The geographical distribution is restricted to a small range, but the species population numbers can be high. The second factor is based on habitat specificity, but it is restricted to specific habitats as the extensive range of species can be found when the habitats are specified. The third one is based on population size (small population size) (Hunter *et al*., 2012).

1.2.21. Conservation of agriculture biodiversity

To conserve agriculture biodiversity or plant genetic materials, two approaches have been proposed. The first one is *in-situ* conservation, which refers to the conservation of plant genetic materials in their original geographic location in which they belong and their distinctive property that has developed over the years (CBD, 1992). *In-situ* conservation can be done in protected areas. A protected area is a geographical area

that is built to archive one particular conservation aim or more (CBD, 1992). *Ex-situ* conservation is the method that involves conserving species outside their natural surroundings. It could be done in gene banks, botanic gardens or another environment. Crop wild relatives are parts of agriculture biodiversity as when conserved they contribute to food security and contribute to increasing agriculture production directly or indirectly. There is always a scientific debate on where species should be conserved. Is it *in situ* or *ex situ?* A group of scientists supports *in-situ* conservation where species adapt to their natural environmental conditions where they can continue to thrive. This approach is particularly important as with climate change their theory that species will adapt to the new conditions. In this Ph.D. study, this approach will be focused on more. And there is another group of scientists that support *ex-situ* conservation as genetic resources are preserved safely and stored in good storage conditions. So, in the event of a natural disaster or climate change, plant genetic resources can be withdrawn and planted again. Examples of *ex-situ* conservation are national gene banks and the international seed vault in Svalbard in Norway. The number of seed samples stored is 933,304 as accessed on September 2017 (NordGen, 2017). The International Centre for Agricultural Research in Dry Areas (ICARDA), which works in the Fertile Crescent, deposited 93,571 accessions in the seed vault as of September 2017 (NordGen, 2017). Once established, the seed vault is believed to be a preservation centre in case of climate change after a hundred years. However, due to the war in Syria, the vault was open and 38,073 samples of seeds were withdrawn from it by ICARDA and sent to Morocco for replanting (Global Crop Diversity Trust and ICARDA, 2015).

As both conservation methods have been outlined, it is believed that both approaches should be done together and that they complement each other. The seed vault in Norway contains CWR from the Fertile Crescent and there are other centres that host CWR. The seed vault in Norway is an example of *ex-situ* conservation. For *in-situ* conservation, Stolton and Dudley (2010) stated that there are 105 protected areas internationally that have CWR. Up to recent times, there have not been many cases of genetic reserve administration strategies with the inclusion of certain CWR practices. Hunter *et al*. (2012) state that there are no reserves aside from the Erebuni Reserve in Armenia and limited reserves for wild fruit trees that are considered *in-situ*

preservation of crop wild relatives. The Erebuni Reserve in Armenia has wild wheat and was created in the eighties (Hunter *et al.*, 2012). It is only in the last 10–15 years that some serious attention has been drawn towards the conservation of CWR in their natural habitat. While it is necessary to protect CWR in protected areas, several ecologists and biodiversity researchers have identified the demand for preservation outside the borders of formal protected areas (Franklin, 1993; Wear *et al.*, 1996; Miller, 1996; Reid, 1996; Chapin *et al.*, 1998; Daily *et al.*, 2001; Rosenzweig, 2003).

Having studied CWR in the Fertile Crescent, it is important to look at the current location of protected areas that are known to have CWR in the Fertile Crescent. Different resources from different countries have been looked at, for example in Syria the protected area that was established between Sale and Rashida has high concentration of wild wheat (Amri *et al*, 2005). In Palestine, there was an initiative to practise an *in-situ* site for crop wild relives in Wadi Sair (Al-Atawneh *et al.*, 2005). The site is a privately-owned farm. The site comprises Medicago species as well as Vicia and Trifolium. The density of the CWR population varies in the site. The site is now monitored by the local government as it contains important plant genetic resources (Al-Atawneh *et al.*, 2005). In Israel, the task of conserving crop wild relatives is done by universities and governmental institutions. There is the Israeli gene bank which contains several seeds of crop wild relatives. The University of Tel Aviv alone preserved 8,000 accessions of wild relatives of barley (FAO, 1996). Amniad reserve has *Triticum dicoccoides* and other crop wild relative species (Anikster *et al*., 1997). *In-situ* conservation of crop wild relatives was done in a project supported by the government in Turkey in the Bolkar Mountain. The project aims at conserving crop wild relatives of Triticum, Hordeum, Cicer and Lens species. In Turkey, in Antalya, there are CWRs for broad beans conserved *in-situ* in Beydaglari (Mulongoy and Gidda 2008). *Ex situ* conservation in Turkey is done through gene banks. It is estimated that 20,000 samples are preserved in gene banks in Turkey belonging to 2,221 CWR (Guloglu, 2017).

After examining all major *in-situ* sites in the Fertile Crescent, a map was created that shows protected areas that have CWR in the Fertile Crescent. The result can be seen

in Figure 1.17. Different colours represent different protected areas in different countries.

Figure 1-17. Protected areas known to have CWR in the Fertile Crescent created using ArcGIS Pro 2.4.

For other countries of the Fertile Crescent, crop wild relative conservation activities vary. In Iraq, not much documented work has been done for *in-situ* conservation. However, there is a new initiative by the Royal Botanic Garden in Edinburgh and Nature Iraq to do some *in-situ* work (RBGE, 2017). For *ex situ*, seed samples have been taken from around the country and preserved in gene banks. The work has been done by the Iraqi Ministry of Agriculture. Around 320 accessions of wild wheat and 50 wild barley were collected and preserved (FAO, 2007). In Lebanon, *ex situ* conservation is done through ICARDA as the ICARDA offices moved from Aleppo to Beirut. There are 1,969 accessions in ICARDA from Lebanon. Around 355 accessions are preserved in gene banks in Europe. There is also ongoing *in-situ* work initiated by the American University of Beirut (AUB) as well as ICARDA and the Lebanese Agricultural Research Institute (Chalak and PGRFA, 2015).

In 2003, it was acknowledged that only approximately 10% of the Earth's surface is identified as protected areas (WRI, 2003), and a part of this partition deals with the lands used for various purposes other than conservation of wildlife and natural habitat. Such areas were recognised for either their natural beauty or profitable values (Pressey *et al*, 1997; Scott *et al*, 2001). It is necessary to consider conservation practices on lands outside the boundaries of protected areas such as agricultural land and landscapes. Even though some land users noticeably dislike some conservation objectives, many components of biological diversity can cope with some degree of unwanted human invasion and modification of the natural landscape (Redford and Richter, 1999; Currie, 2003). Polasky *et al*. (2001) argue that political opposition arises when conservation plans are high in cost, and thus are unlikely to be adopted and implemented. Socioeconomic and political pressure limits the size of areas that need to be protected. Polasky *et al*. (2001) suggest that preservation outside of the genetic reserves is a less costly alternative to using the approach of protected area selection. This assumes that species stay alive only in the interior of protected areas and economic practices exist only beyond the boundaries of a natural reserve. It is important to look at the soil seed bank to conserve these species either outside or inside the protected areas (Polasky *et al.*, 2001).

1.2.22. Protected areas

1.2.22.1. Turkey

Turkey has declared 40 state parks, 31 nature preservation zones, 107 monuments, 184 flora and fauna parks, 81 wildlife protected zones, 58 forest preservation sites, 239 genetic preservation zones, 373 seed banks ad 15 specific protected areas (Kucuk and Erturk, 2013).

1.2.22.2. Syria

Syria has declared 24 protected areas accounting for 1.29% of its total land area. It has five marshlands, one wildlife site, three aquatic protected zones and 13 forest sites (Abido, 2010).

1.2.22.3. Lebanon

Lebanon has declared 13 nature reserves, 18 protected forests, and 17 protected sites, many of which have also acquired international designations including Ramsar

sites, Special Protected Areas of Mediterranean Importance, Important Bird Areas, and World Heritage (Ministry of the Environment in Lebanon (MOE), 2016).

1.2.22.4. Iraq

The area covered by existing and proposed nature reserves is around 2,440 km^2. It represents around 0.65% of the country's area. The country has declared one proposed national park, one established other type of PA and one established Ramsar Site (Hawizeh Marsh) (Al-Lami, 2012).

1.2.22.5. Palestine

There are 10 existing nature reserves in Palestine. There is a proposed nature reserve in Wadi Gaza and eight nature reserves proposed by the Israeli side (MOE, 2016).

1.2.22.6. Jordan

There are seven main protected areas in Jordan. Dana Biosphere Reserve is the largest in size (320 km^2). Mujib Nature Reserve is the lowest nature reserve in the world (RSCN, 2016).

Institutes that hold information on the Fertile Crescent crops and their wild relatives

There are several national and overseas institutes including Germplasm banks, herbaria, universities, and botanical gardens that host a wide number of Fertile Crescent crops and their wild relatives. These sources include Global Biodiversity Information Facility (GBIF), (GRIN), the Herbarium Catalogue Kew, Natural History Museum London, New York Botanic Garden, GENESYS, JSTOR Global Plants Harlan and de Wet Inventory.

1.3. FOOD SECURITY

Food security can be obtained once "there is physical and economic access to nutritious and safe food and sufficient quantity to every person in order to maintain a healthy and active life" (FAO, 2007).

One in 9 nine people worldwide has insufficient nutrition supply to maintain a good and balanced health. One out of six children, roughly 100 million, in developing countries is underweight and around 16% of childhood malnourishment is found in developing countries (FAO, 2015).

In the Fertile Crescent, the statistics are alarming. In Iraq, the proportion of the total population (2014–16) that are undernourished is 22.8%. The number of people undernourished from 1990–92 was 1.4 million, in 2000–02 it was 5.8 million, in 2005–

07 it was 7.3 million, in 2010–12 it was 7.8 million, and between 2014–2016 it was 8.1 million. In Syria, the amount of starvation in the whole populaces from 2014 to 2016 was 5–14.9%. In Palestine, the amount of starvation in the whole populaces was 25–34.9%. In Jordan, the amount of starvation in the whole populaces from 2014 to 2016 was <5.0 %. In Turkey, the amount of starvation in the whole populaces from 2014 to 2016 was <5.0 %. In Lebanon, the amount of starvation in the whole populaces from 2014 to 2016 is <5.0% (FOA, 2015).

1.3.1. Food security by country

1.3.1.1. Syria

The whole of Syria is food insecure. One-third of its population, greater than 6,000,000 individuals, do not have enough food. What varies geographically is its severity and the extent to which it is influenced by external circumstances (WFP, 2015). The situation is worst in Aleppo, Rural Damascus, Al Hassakeh, Hama, and Dara governorates, where more than 40% of people are food insecure. Food insecurity is higher in rural than in urban areas (Figure 1.18). This is to be expected as the rural economy is dominated by agriculture, but the crisis has affected the rural sector, and agriculture no longer contributes as much as it did before the crisis (WFP, 2015).

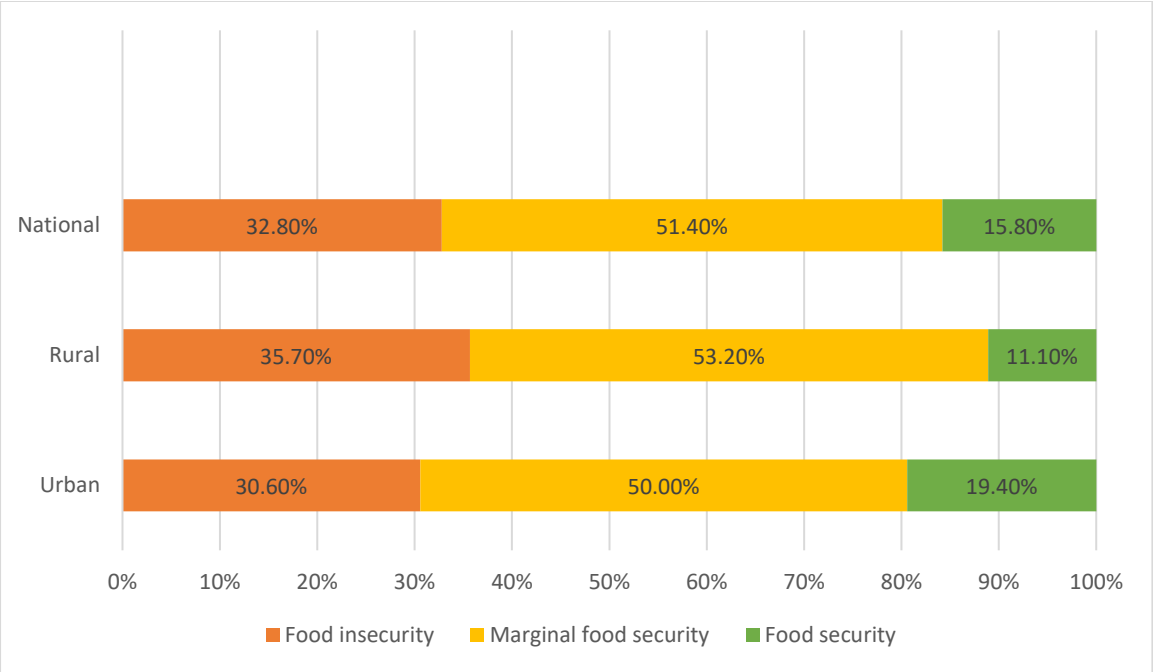

Figure 1-18. Food insecurity in Syria reproduced from WFP (2015)

1.3.1.2. Palestine

The food security survey that was done in 2013 indicated that 1.6 million people in Palestine (Figure 1.19) suffer from food insecurity. This high level accounted for a third of the population at the time of the study (PCBS *et al*, 2014).

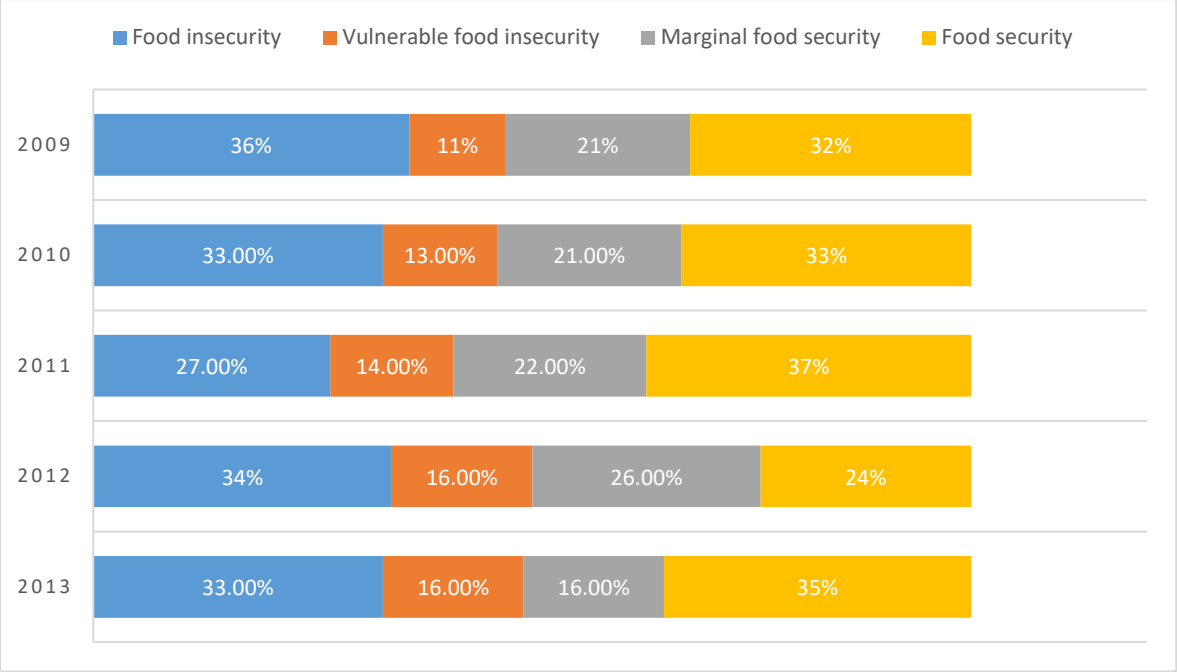

Figure 1-19. Prevalence of food insecurity in Palestine, 2009–2013 reproduced from PCBS et al. (2014)

1.3.1.3. Lebanon

As can be seen in figure 1.20, around 42% of the households in the southern part of Lebanon and 62% of refugees from Palestine are food insecure (Sayhoun *et al*., 2014).

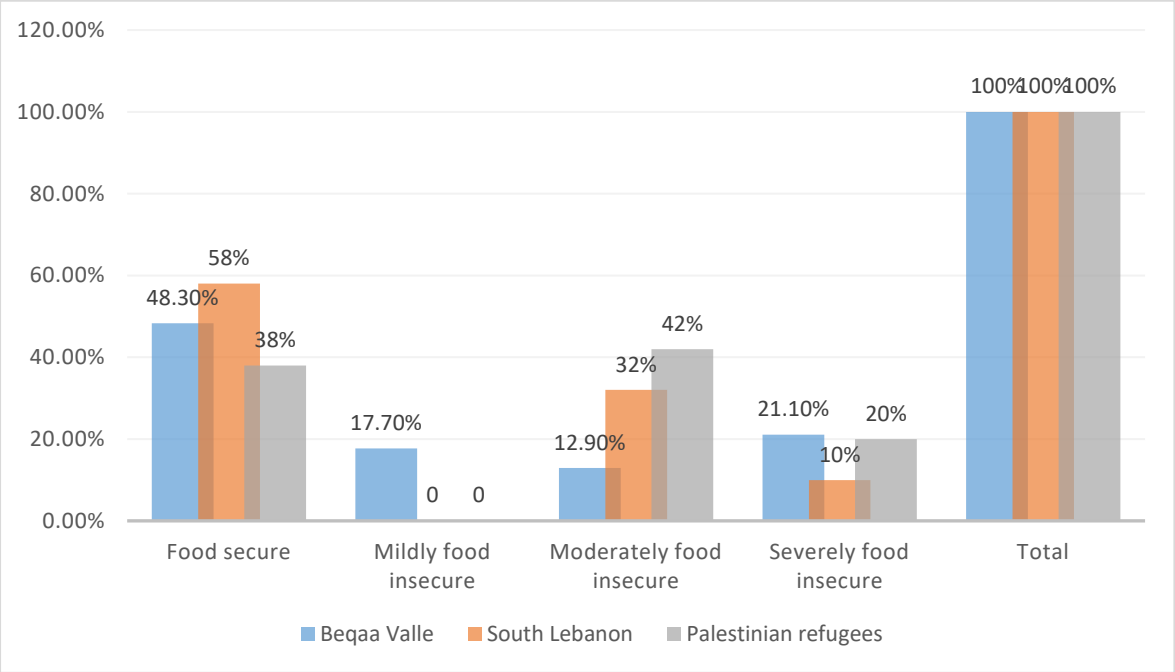

Figure 1-20. Food security prevalence among Lebanese subpopulations reproduced from Sayhoun et al. (2014).

1.3.1.4. Iraq

Years of wars, financial crises, and the conflict has had a severe impact on the quality of life for the Iraqi population. The number of unemployed people increased and the number of poor increased. The level of food insecurity increased. There are two series of areas that have a high level of food insecurity. The first area contains 28 districts with 5,800,000 citizens living there. The poverty in these districts is extreme with extreme malnutrition. The second area contains eight districts with 1,400,000 citizens living there. The level of malnutrition in these districts is high with 34.8% of the population having chronic malnutrition and a 13.8% wasting level (WFP, 2004).

1.3.1.5. Jordan

As can be seen in Figure 1.21, 63.9% of the population in Jordan are food secure (WFP, 2012).

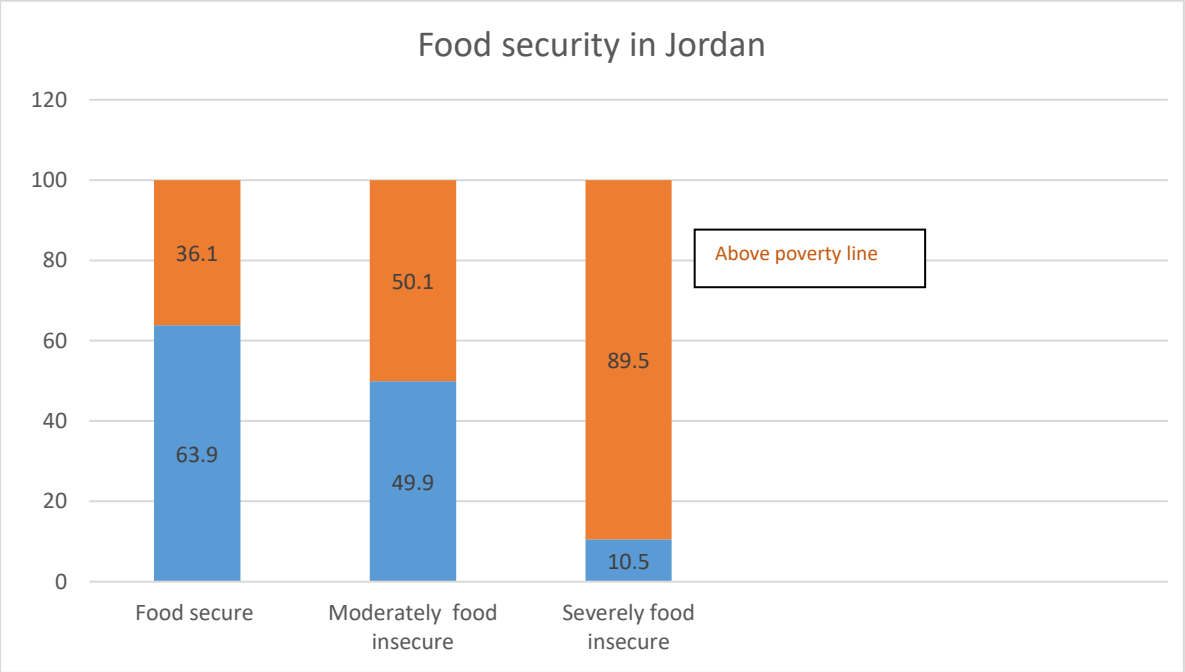

Figure 1-21. Food insecurity prevalence in Jordan reproduced from WFP (2012)

1.3.1.6. Turkey

Based on the Turkish Nutrition Country Profiles report that was made by FAO in 2001, it seems that the population in Turkey are very well nourished. The average energy consumption was calculated and it is 3,500 kcal per capita a day. Protein supply per person was determined as the top. The Nutrition Country Profiles report did not illustrate well the food poor quality that is consumed in Turkey (FAO 2001).

1.3.2. Human population

Human population is increasing rapidly. The annual human population growing degree is projected to decline from 1.18 to 0.5 by 2050, but the population will be around 9.7 billion by the same year (UN, 2015). To provide food for such a high number, there will be a massive need for goods and services as well as areas for agriculture. To meet such huge needs yield must rise by 70% of the current worldwide amount and from 77%–100% in underdeveloped countries (Alexandratos and Bruinsma, 2012). Around 73% of the food supply would come from yield rises, 21% from expanding areas suitable for agriculture and 6% from intensifying agriculture (Alexandratos and Bruinsma, 2012). Climate change may have a drastic influence on crop productivity (IPCC, 2014). Figure 1.22 shows human population in the Fertile Crescent countries.

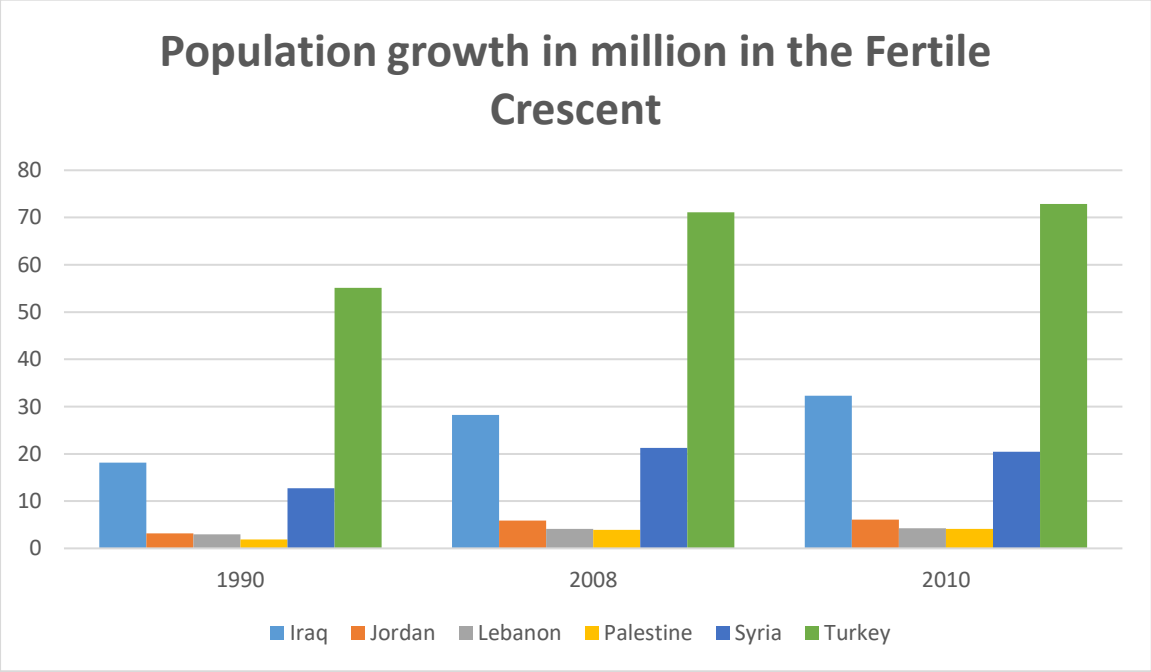

Figure 1-22. Human population in the Fertile Crescent countries in 1990, 2008 and 2010 based on information from the World Bank (2016)

1.4. CONTEXT

1.4.1. Crop wild relatives

The genetic pool of our main food crops is limited. There are only a few varieties that farmers can choose from for cereals, legumes, vegetables, and fruit. The larger list of varieties, the better it is for farmers as they will have a better chance of selecting a better variety that suits their requirements, especially now with increasing consumer

demands for better quality crops which drive supermarkets to set high standards which puts more pressure on farmers so they have to meet their high standards. To illustrate the limited genetic pool of our main crops, studies on genetic diversity in the Fertile Crescent were conducted. Bishaw (2015) did a survey and found out that for wheat, farmers only grow five main varieties including Cham 1, 3 and 6 on 81% of wheat fields and for barley farmers grow one main variety in Syria (Bishaw, 2015).

Another important factor is that insects developed resistance toward pyrethroid pesticides (Chen *et al.*, 2017) and many of the pesticide are coming off the market due to their toxicity profile either secondarily or directly, and their leaching into drinking water (Jaipieam *et al.*, 2009) so water companies are rushing to ban these chemicals in order to prevent them getting them to consumers with tap water. An example of that is the ban on the pesticide imidacloprid due to it is toxicity to bees. Also, lots of resistance toward fungicides can be seen (Dolores *et al.*, 2017). Weeds are becoming less susceptible to herbicides (Green *et al.*, 2011). In summary, there is a huge demand to develop new varieties that are resistant to insects, pests and diseases, and varieties that can compete more on the soil with weeds. There is also demand for varieties with better quality that could meet supermarkets' high standards and demands with no ergot or *Fusarium* in the case of wheat and barley and no scape and blights for potato. There is also a demand for producing crops with less MRL (mg per kg) of pesticide residue as recommended by the Health and Safety Executive in the UK (HSE, 2017) or the EU MRL directive (EU, 2017). There is also a demand for varieties that withstand certain conditions in different parts of the world. In the Fertile Crescent context with its huge water problem, Israel was ranked the poorest in water availability all over the world (OECD, 2016). Alongside pests and diseases, there is a demand for varieties that have less water demand and can tolerate soil salinity as not all the Fertile Crescent has perfect soil conditions. Arable land amounts to 35,121,000 ha (Nationmaster, 2005) and the soil fertility varies (Figure 1.24).

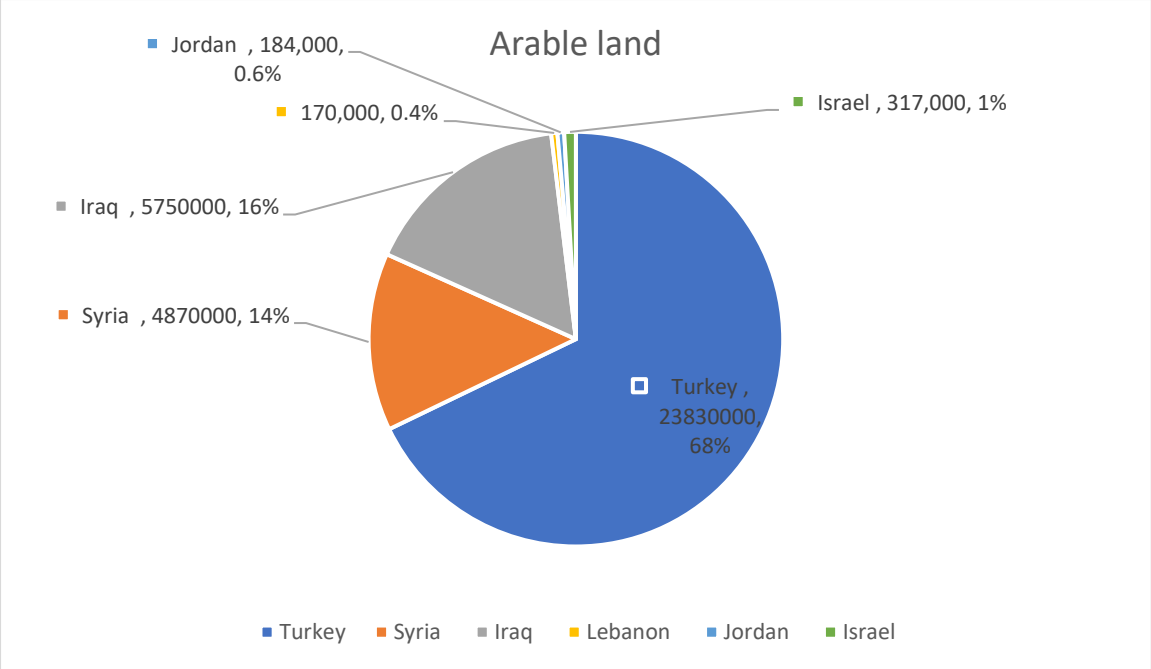

Figure 1-23. Arable land in the Fertile Crescent countries based on data obtained from Nationmaster (2005)

That is why there is a huge demand to broaden our crop varieties and safeguard the genetic materials of crop wild relatives. Gene transfer is the main drive for conserving crop wild relatives' genetic resources and trying to safeguard them. However, there are other factors to conserve them as some of them have a medical value such as *Vicia angustifolia* L. which is used for lessening coughs (Bahmani *et al.*, 2014) and it is closely related to *Vicia faba*. Some CWR have a cultural value, such as *Cedrus libani* in Lebanon (Hawkes *et al.,* 2000) and it is on the Lebanese flag. The crop wild relative of barley, *Hordeum spontaneum,* demonstrated a high level of resistance to drought in a field experiment (Lakew *et al.*, 2011). The wild relative of wheat (*Aegilops ventricosa*) is resistant to Eyespot (Mena *et al.*, 1992). The gene that is responsible for the resistance is Pch 1. Pch 1 was transferred to KWS Zyatt which is a wheat variety (Mena, 1992). Eyespot can cause 10 to 30% yield decline in winter wheat (AHDB, 2012). Vavilov (1926) realised the significance of crop wild relatives and their role as genetic materials for crop improvements. He started collecting crop wild relatives of major crops from around the world. He collected samples of corn with different varieties (Vavilov, 1926). So, what are crop wild relatives and how close are they to cultivated crops? Crop wild relatives are plants that are closely related to cultivated crops. Cultivation was mentioned, not domestication, as cultivation is the

stage after domestication. So CWR has value as plant genetic materials that are used and have the potential to be used in improving our current crop varieties through introducing new genes and solving a particular problem either resistance or tolerance (Maxted *et al.*, 2006). Therefore, CWR improve our current varieties and can be used to create new varieties (Tanksley and McCouch, 1997). Moreover, CWR have a border genetic diversity compared to the associated crop (Vollbrecht and Sigmon, 2005), and this is due to their being in a more stressed environment than the associated crop, as crops in the field or greenhouses have the near-perfect environment created for them by humans. These vary from good nutrition and crop protection as well as irrigation, whereas CWR are left in the wild exposed to urbanisation, pollution and soil degradation. Consequently, CWR are crossed with each other and have developed anti-stress genes over the years (FAO, 1998, 1998, 2010).

The degree of relatedness of CWR and a crop can be determined using the gene pool model. This model was developed by Harlan and de Wet in 1971. The degree of relatedness of CWR can be also established by the Taxon Group principle proposed by Maxted *et al.* (2006). Both methods determine how close the CWR is to the associated crop genetically. It is important to determine how related the CWR is and accordingly it can be determined whether it is easy, difficult or impossible to cross or transfer the desirable genes from the CWR to an associated crop. Another reason why it is important to determine how close the CWR is to a cultivated crop is that it helps in the prioritisation process of selecting the priority list for conservation. Moreover, the degree of relatedness is important in taxonomy as well. Harlan and de wet's (1971) concept is that biological species are divided into three main categories based on their degree of relatedness (Harlan and de Wet, 1971). In our case, plants as part of the biological species and gene pool 1 contain the cultivated crop represented by varieties. Gene pool 1 is divided into two groups: gene pool 1 A, which contains crop varieties, and gene pool 1B, which contains spontaneous races (Harlan and de Wet, 1971). Crossing between gene pool 1 A and B is done successfully through classical plant-breeding methods. The other category is gene pool 2, and members of this category can cross freely with members of gene pool 1 using the classical plant-breeding methods. However, there are some genetic barriers between the two groups. Therefore, the first generation may be poor due to weak chromosomal pairing.

Moreover, the future generation may lose the wanted traits (Harlan and de Wet, 1971). Members of gene pool 3 are far related to cultivated crops and crossing cannot be done freely. It requires *in vitro* techniques to transfer one gene to crop varieties.

Harlan and de Wet (1971) published a figure explaining the gene pool concept and each gene pool represented in a circle. The gene pool figures based on Harlan and de Wet (1971) were reproduced (Figure 1.24). Although there is a distinctive feature between classes, each species is unique and has its own identity. The degree of relatedness is not black and white and there are no definite classes, but it is a percentage. In biology, the class between gene pools is a percentage and that is why there is a need to create the gene pool pyramid. Gene pool 1 is in the top of the pyramid with both sections A and B. Species within these crops might be a bit closer or more distant, but the general features of the two groups are the same (crop variety for group A and wild or weedy for group B). How much is the species related to the cultivated crop represented in the small triangles and percentage from 0 to 100%? The top of the pyramid represents gene pool 1, the bottom is gene pool 3 to the left and gene pool 4 is to the right. Gene pool 4 is added to the classification to represent species which are distantly related.

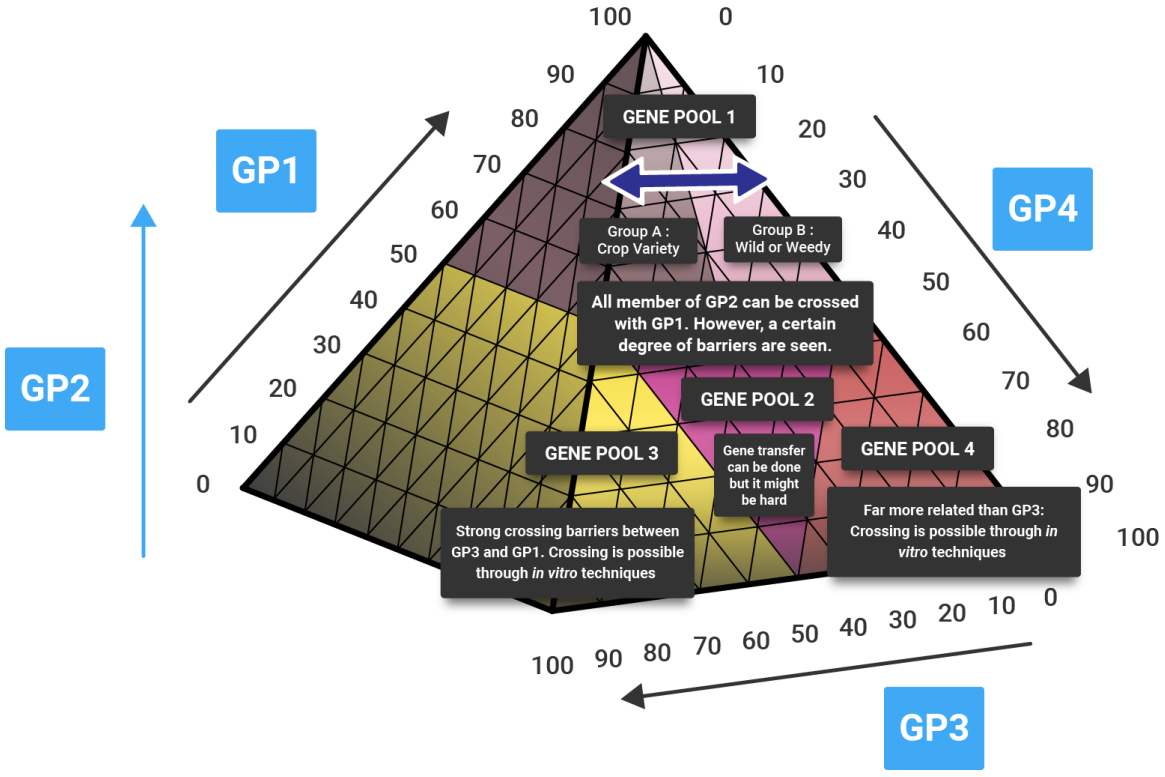

Figure 1-24. The gene pool pyramid adapted from Harlan and de Wet (1971)

In prioritisation, when not much information is present about the gene pool of the taxa, then the Taxon Group methods will be applied. The Taxon Group method is proposed by Maxted *et al.* (2006) and contains five main categories. It is based on how species are related inside the family. Taxon category one, for example, is divided into category A which contains the crop variety. Category B represents the same species and that is why it is a wider category. Category 2 represent the same section. Category 3 represents the subgenus. Category 4 represents the genus. Category 5 represents the same tribe but different genus (Figure 1.25).

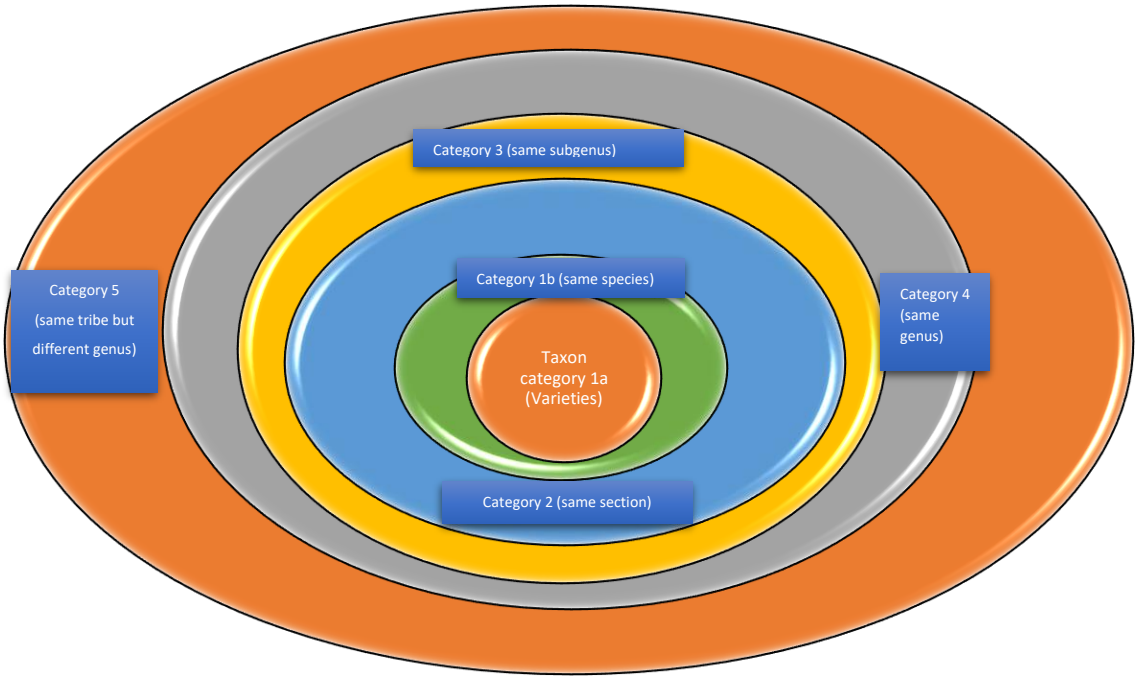

Figure 1-25. Taxon categories reproduced from Maxted et al. (2006)

Based on the gene pool criteria and the taxon category, a CWR when found in the wild can be classified in one of these categories and consequently how difficult or easy to cross with the associated crop can be defined. For example, if the CWR is in gene pool 1b, crossing is easy with the associated crop and the CWR can be used for gene transfer. If the CWR is in taxon category 5 then it is difficult to transfer the desired gene to the associated crop. These categorisations are also essential in prioritisation. CWR have more priority if they are closely related to the crop as it is easy to transfer the genes. Gene pool 2 has more priority than gene pool 3 and taxon category 1b has more priority than 2.

1.4.2. Value and utilisation of CWR

Crop wild relatives have also been a supply of genetic diversity for crop improvements, such as providing resistance against many insects and plant diseases. Pimentel *et al*. (1997) estimated the annual global value of CWR gene introductions in enhancing crop production and found out that it is around 115 billion USD. PricewaterhouseCoopers (2013) estimated the potential value for the CWR of 32 main crops to be 196 billion USD (PricewaterhouseCoopers, 2013). A study on the utilisation of crop wild relatives in global crop enhancement programmes by Maxted and Kell (2009) stated that there are at least 183 CWR that have been used for crop improvement in relation to 29 crop species that are considered as significant for ensuring food security (Maxted and Kell, 2009).

During the screening of wild emmer wheat (*Triticum turgidum* subsp. *dicoccoides*), a broad genotypic variability was noticed and the level of minerals such as Zn and Fe as well as amino acids two times more in the CWR compared to the cultivated crop (Chatzav *et al.*, 2010). According to this study, the wild emmer germplasm was considered to provide unique opportunities for the exploitation of good alleles for improving the wheat minerals and protein contents that were previously absent in the cultivated wheat (Chatzav *et al.*, 2010).

Certain ideas on the level of value may also be derived from the available estimations with reference to the particular plants. For instance, the beneficial qualities of CWR of sunflower (*Helianthus* spp.) have a value of around $267 to $384 million per annum to the sunflower farming in the US (Seiler et al, 2017).

A CWR of tomato has provided a rise of around 2.5% in the dry matters of tomato, costing 250,000,000 USD. Three CWR helped develop peanut cultivars that are resistant to *Meloidogyne* species causing root damage and costing farmers $100,000,000 annually. The financial involvement of most of the crop wild relatives has been observed on a smaller scale (Hunter and Heywood, 2011; PwC, 2013). Some excellent cases are the crop wild relatives of common wheat including the Aegilops species. For example, *Aegilops variabilis* Eig has bred with *T. aestivum* cv., “Rusalka”, for the purpose of creating a powdery mildew-resistant wheat (Spetsov *et al.*, 1997).

Lakewa *et al.* (2011) state that *Hordeum spontaneum*, a wild relative of barley, can be used in crop improvement as it has genes that showed high performance under drought stress conditions.

Barley is an important crop in the Fertile Crescent. In 2014, the total area harvested in the Fertile Crescent is 5,150,635 ha (FAOSTAT, 2017) (Table 1.3).

Table 1.3. Barley area harvested in Ha and yield hg/ha in the Fertile Crescent countries based on the FAOSTAT (2017) database.

Country	Area harvested in Ha	Yield hg/ha
Iraq	1,145,814	11,152
Israel	6077	24,683
Jordan	38,139	10,192
Lebanon	18,605	17,737
Occupied Palestinian Territory	8,568	15,830
Syrian Arab Republic	1,220,559	4,917
Turkey	2,718,950	23,171
Total	5,156,712	107,682

In Syria, for example, there are two main barley varieties that growers recognise: the white seeded and black seeded. The white seeded grow in areas from 250 to 400 mm and the black seeded grow in less than 250 mm (Ceccarelli and Grando, 2000). The yield of barley in the Fertile Crescent is very low. To determine if it is low or high, the yields have been compared with the yield in the United Kingdom which is 63,991 hg/ha based on FAOSTAT (2017). The yield in the United Kingdom is around 6 times more than the yield in Jordan or Iraq. One of the reasons for the low yield is that barley in the Fertile Crescent depends on rain feed. To increase the yield, farmers should use more drought-tolerant varieties. One of the solutions would be to identify crop wild relatives of barley that are drought tolerant. ICARDA identified two crop wild relatives of barley *Hordeum spontaneum* 41-1 and 41-5 that are drought tolerant (Lakew *et al*., 2013).

CWR have been found to be distributed in many locations. Many pieces of research have revealed a continuous degradation of worldwide habitat putting the existence of these economically significant species at danger. The IUCN and the European

Commission recently produced a plan that provides a European Red List. The 572 selected native European wild relative crops have a high value for human and animal food. The assessment found that *Allium jubatum* J.F. *Macbr* is extinct, 11.5% (66 species) of the total species have been listed as threatened in the European region, 3.3% (19 taxa) are critically endangered, 4.4% (22 taxa) are endangered, and 3.8% (25 taxa) are vulnerable. About 4.5% (26 taxa) are recorded as near threatened (Bilz *et al.*, 2011; Kell *et al.*, 2012). The rest is data deficient (29%) and of least concern (54.7%). Among the species classified as least concern, around one-third of them have been listed as threatened nationally (Kell *et al.*, 2012). For this reason, there has been a huge demand for threat assessment. In the Fertile Crescent region, there is a Red List assessment that was done for plants in Jordan. Nearly 40% (1,072 species) of the flora in Jordan was Red List assessed. The assessment found that 106 species of the total species have been listed as threatened nationally with 19 species of them being critically endangered, 54 species being endangered, 33 as vulnerable and one species (*Salvia farinacea*) as regionally extinct (Taifour and El-Ohlah, 2014).

1.4.3. Global significance of the Fertile Crescent biodiversity

The Fertile Crescent is an essential region for safeguarding global food security (Keisa *et al*., 2008). In the Fertile Crescent, CWR diversity is declining and also climate change will impact negatively on their diversity. Therefore, it is necessary to conserve CWR in the region through both using GIS tools and conserving them *ex situ* to contribute to food sustainability (Keisa *et al*., 2008).

ICARDA (1995) states that the “Fertile Crescent” used to have a balance achieved between the natural ecosystem and human. Unfortunately, this balance has been disturbed to a larger extent and is expected to be further disrupted by the increasing population on a diminishing and over-used resource base (ICARDA, 1995).

Nearly 60% of the ecosystem’s services, including CWR, are being degraded or used in an unsustainable manner. This often results in significant harm occurring to the well-being of humans (Millennium Ecosystem Assessment (MEA), 2005), which leads to the emergence of an urgent need for reversing the loss caused to these environmental resources, particularly biodiversity.

Substantial literature reviews by researchers such as Tukan *et al*. (1998) and Aburjai *et al*. (2007, 2010) affirmed the role of CWR in ensuring the income and subsistence

for communities residing in marginal areas. A review of global ecosystems in the Millennium Ecosystem Assessment (MEA) (2005) highlights biodiversity conservation in relation to the wild plant's conservation and poverty reduction. It can be concluded that there is a concentration of CWR in the Fertile Crescent that is of global importance. There are areas of potential growth for their macro-economic participation in areas such as food security and medicine. With these combined factors, it can be assumed that there is a greater relevance in developing regions and this contributes towards the improvement of the livelihoods of the communities and the success of their respective governments (Bushuk, 2001).

1.4.4. Conservation of CWR

Conserving the occurrence places of CWR in their natural environment will result in the preservation of a wider amount of related species. It will lead to conservation of a broader percentage of the biological diversity across and within a gene pool. Moreover, the ongoing adaptation to climate change in species' natural surroundings and resistance to potential pests and diseases are not interrupted. Regardless of these advantages of *in-situ* conservation, natural disasters, land use changes, and other factors are potential threats that could impact the accomplishment of any CWR conservation strategies (Maxted and Kell, 2008). Applying complementary methods for crop wild relatives' genetic resources, preservation will guarantee effective crop wild relatives' preservation and reduce the threat of declining valued genetic materials (Maxted and Kell, 2008). There are efforts from ICARDA to conserve CWR from the Fertile Crescent *ex situ* through collecting CWR seeds and distributing them. In the ICARDA gene bank, there are around 148,000 accessions, most of them CWR related to wheat, barley, pulses and other important crops. Around 80% of these accessions are duplicated in the Seed Vault in Norway (ICARDA, 2017).

1.4.5. Regional CWR conservation strategies

In order to identify the principles of CWR conservation at different levels (e.g. local, national, regional, global), strategies and an action plan must be conducted in a harmonised and systematic manner. A conservation strategy for CWR can be defined as the complementary *in-situ* and *ex-situ* series of actions that can be done systematically and co-ordinately (Figure 1.26). The major aim of such strategies is to

achieve an active preservation and utilisation of biological diversity of CWR genetics and taxonomy for the long term (Maxted *et al.*, 2013).

A regional crop wild relatives preservation plan for the Fertile Crescent assesses the existing preservation actions of crop wild relatives and potential frameworks for safeguarding these vital CWR resources with the involvement of various stockholders and local governments.

All data, analysis, and outcomes are put forward collaboratively in a report as guidance for organisations and authorities to evaluate the human and financial resources needed for the implementation and maintenance of these preservation activities (Maxted *et al.*, 2013).

In principle, a regional crop wild relatives preservation plan will include: a) the formation of a checklist for the regional crop wild relatives as well as an inventory of the priority taxa that exist within a region, b) occurrence data of prioritised CWR taxa, c) a genetic diversity study of these taxa, d) threat analysis for the CWR priority list, e) finding principal locations for CWR preservation, f) creating preservation aims, objectives, and schedules, and g) applying, observing, and promoting CWR preservation activities (Maxted *et al.*, 2013) (Figure 1.26).

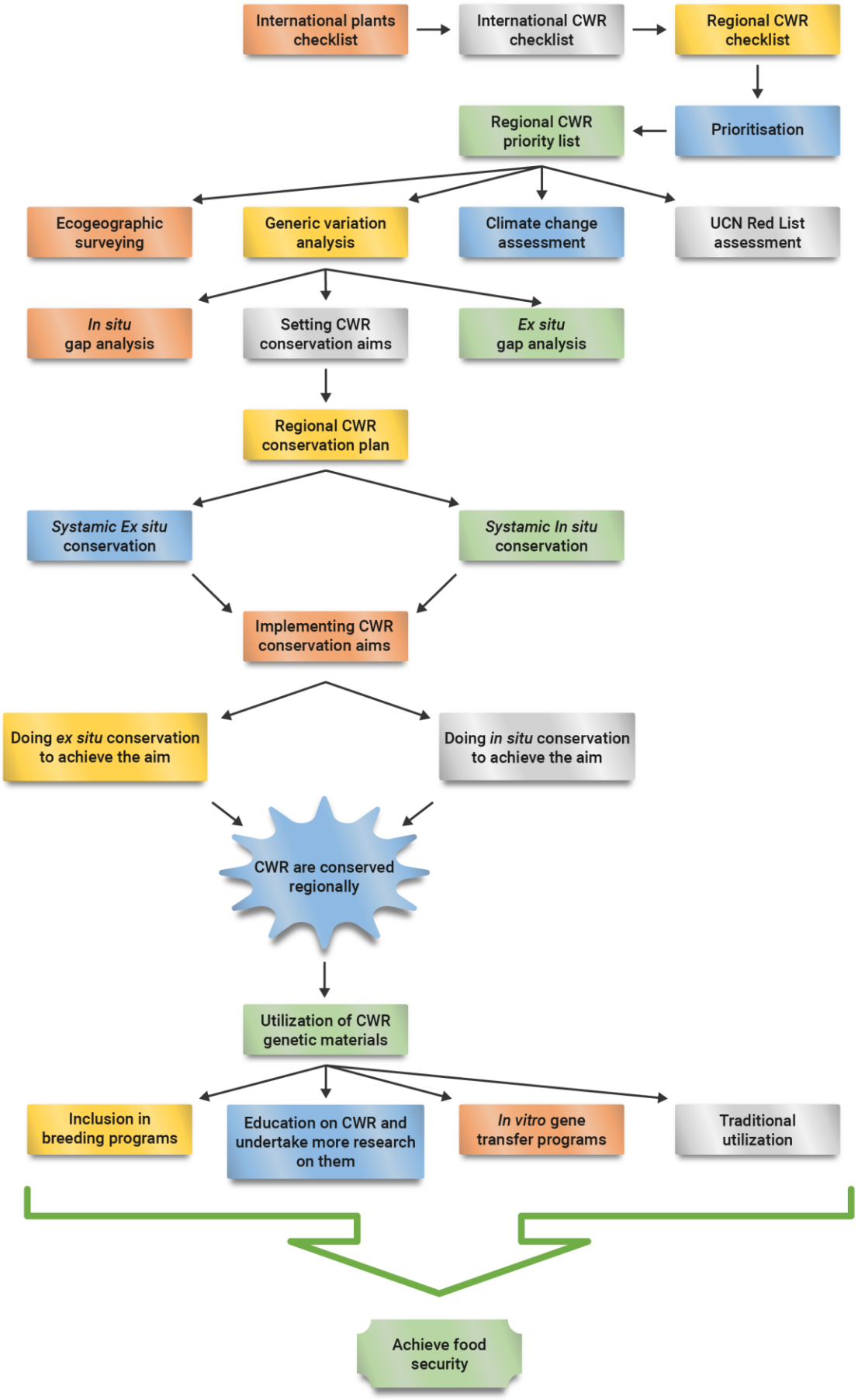

Figure 1-26. Model for the development of a regional management plan for CWR conservation (adapted from Maxted et al., 2013)

As can be seen in the Figure 1.26, creating a priority list is an important step to conserve crop wild relatives in the Fertile Crescent. The regional conservation is different from the national conservation as first of all the boundary of the region needs to be established. In this study, the boundaries of the study area were established which is the Fertile Crescent. Then a plant checklist for the region should be established. Next, a CWR checklist should be created after removing the domesticated crops from the list. After that, prioritisation should be given to the most important CWR, consequently establishing a CWR priority list for the region.

1.4.6. The study goals and objectives

1.4.6.1. Goal

The goal of this research is to analyse the biodiversity of the major representative crops and their CWR in the Fertile Crescent and the development of a systematic CWR conservation strategy for these genetic resources as an aid to underpinning global food security.

1.4.6.2. Objectives

To achieve this aim there are subordinate research objectives:

Development of a proposal for regional CWR conservation actions for the Fertile Crescent. A proposal will be put forward for CWR conservation actions for the Fertile Crescent as a mega-region of agrobiodiversity, which will involve a monographic approach to CWR conservation including:

a. Generation of a regional inventory of CWR, prioritisation based on agreed criteria.

b. Collation of additional regional information (for example, occurrence data, IUCN risk status, gene pool information).

c. Find possible locations for CWR preservation.

d. Climate change study of CWR. A study on the possible effects of global warming on the distribution of CWR will be developed.

e. CWR threat analysis. Undertake CWR threat analysis to assess the risk of genetic erosion facing CWR across the Fertile Crescent. This will involve a IUCN Red Lists assessment of CWR taxa to determine their level of threat of genetic erosion.

1.4.6.3. Project products

1. An inventory of CWR of the Fertile Crescent.
2. Proposed sites for CWR conservation in the Fertile Crescent.

3. Climate change analysis of CWR in the Fertile Crescent.
4. Threat assessment of CWR.

2. CHAPTER 2: SETTING CONSERVATION PRIORITIES FOR CROP WILD RELATIVES IN THE FERTILE CRESCENT

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Author contributions: Wathek Zair collected the data. Wathek Zair analysed the data. Wathek Zair wrote the chapter. Nigel Maxted, Ahmed Amri and Peter Winn reviewed the manuscript. Wathek Zair edited the chapter.

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2.2. ABSTRACT

The aim of this paper is to contribute directly to the systematic, long-term conservation of crop wild relatives (CWR) in the Fertile Crescent by setting conservation priorities to secure and improve CWR conservation *in situ* and *ex situ* as a means of underpinning global food security. We established the first priority list of CWR within the Fertile Crescent following several criteria comprising production value, projected production value, production area (ha), projected production area (ha), native status, energy supply (kcal/capita/day), protein supply (g/capita/day), fat supply (g/capita/day), occurrence status, gene pool, taxon group, and threat status. An inventory of 220 priority CWR was established for the Fertile Crescent region. We followed 12 prioritisation approaches and assessed 21,080 species. About 4% of the total species (835 species) were identified as CWR that have socio-economic value for the region. These 835 CWR species were prioritised to create the CWR priority list which consisted of 220 species (1% of the total species assessed). The majority of the CWR priority list (185 species) are related to cereal, vegetable, and industrial crops, and 35 of them are related to fruits and trees. The CWR priority list includes crop wild relatives of the genera *Aegilops* (20 species), *Lactuca* (11 species), *Avena* (11 species), *Carthamus* (11 species), *Allium* (9 species), *Thinopyrum* (10 species), and *Triticum* (3 species). We present the first inventory of 220 priority CWR for the Fertile Crescent. The inventory helps to improve *in-situ* and *ex-situ* conservation and the genetic diversity of CWR. Both the inventory and the methodology applied in prioritisation can be used in setting national, regional, and global conservation

strategies. The recommendations will help the Fertile Crescent meet its targets in conserving CWR diversity as well as making sure that CWR genetic resources are preserved to prevent and tackle global food insecurity.

Keywords: Conservation prioritisation · Food security · Genetic diversity · Plant genetic resources

2.3. INTRODUCTION

The human population is increasing rapidly. It was estimated that the population will reach 11.2 billion by 2100 (UN 2017). That is why there is an urgent need to improve crop varieties so we can produce more food and crops will be able to improve yield, are resistant to insects and diseases, and can tolerate abiotic stress such as high temperature and drought (Araus *et al.*, 2008). Crop wild relatives are species of plants that are genetically close to cultivated crops. They are an important source of plant genetic materials that can be used for crop improvements. CWR have genes that enable them to adapt to various stresses in their natural environments (Maxted et al., 2006). A CWR should be in gene pool one or gene pool two for the gene transfer to be done easily (Maxted et al., 2006). CWRs have been used to improve crops resistant to diseases. For example, in Australia, a crop wild relative of wheat has been used successfully as a source of a gene which is resistant to cereal cyst nematode. The gene from the CWR was transferred to bread wheat (Appels and Lagudah 1990). CWRs have also been used to improve varieties' resistance to stress, such as *Hordeum spontaneum* K. Koch and *Triticum dicoccoides* Körn. the CWRs of barley and wheat have genes that can make them tolerate salty soil and drought (Nevo and Chen, 2010). Crop wild relatives are threatened in their natural habitat; this is due to urbanisation, constructing of roads, deforestation, desertification, intensive farming, erosion of soil and plant genetic resources, pollution of land and water, scarcity of water, overgrazing, and the impact of climate change (El-Beltagy, 2006; Derneg, 2010). Trigo et al. (2010) state that climate change impacted negatively on the vegetation in the Fertile Crescent (Trigo et al., 2010). For all the above-mentioned reasons, there is an urgent need to conserve CWR in the Fertile Crescent and conserve their natural habitats. There are several CWR taxa around the world and the number was estimated to be approximately 50,000–60,000 species worldwide. Of these, approximately 10,740 are a high priority for food security (Maxted and Kell,

2009). In the Fertile Crescent region, a Red List assessment was done for plants in Jordan. Nearly 40% (1,072 species) of the flora in Jordan were Red List assessed. The assessment found 106 species of the total species have been listed as threatened nationally with 19 species being critically endangered, 54 species being endangered, 33 as vulnerable and one species *(Salvia farinacea)* as regionally extinct (Taifour and El-Ohlah, 2014). Authors have used a number of approaches for CWR prioritisation (Maxted et al., 1997; Mitteau and Soupizet, 2000; Barazani et al., 2008; Ford-Lloyd et al., 2008; Maxted and Kell, 2009; Magos Brehm et al., 2010). Magos Brehm et al. (2010) used nine prioritisation criteria (native status, economic value, ethnobotanical value, global distribution, national distribution, *ex-situ* conservation status, *in-situ* conservation status, legalisation, and threat assessment) and applied them to the Portuguese CWR. Species were listed based on their priority from high to low and the top 50 were identified. Those CWR species that were found to be a high priority were given prioritisation for conservation in Portugal (Magos Brehm et al., 2010). While in the United States, Khoury et al. (2013) used crop production and food supply data from the Food and Agriculture Organisation of the United Nations statistical database (FAOSTAT) giving a US priority list consisting of 821 CWR taxa (Khoury et al., 2013). Fielder et al. (2015) applied five prioritisation criteria: use of the related crop, commercial importance of the associated crop, native status, relatedness degree of the CWR to the crop, and latest change in the population to prioritise 148 CWR taxa (Fielder et al., 2015). Other authors when prioritising CWR taxa have used other combinations of prioritising criteria (Barazani et al., 2008), but related crop value, relative CWR relatedness (indicating potential ease of CWR use in breeding), and threat assessment have been used widely. The Fertile Crescent is a very important centre in the plant genetic resources field as it is a centre of crop domestication. Major crops such as wheat, barley, lentils and chickpeas were first domesticated in the Fertile Crescent (Zeder, 2011). The Fertile Crescent is located in Syria, Iraq, Israel, Palestine, Jordan, Lebanon and Turkey (Figure 2.1).

The Fertile Crescent is in the Mediterranean basin region, which is a major region that is known for its great plant diversity. It has between 25,000 and 30,000 plant species (Heywood 2003). Vavilov (1926) located crop origin centres in the world where crops originated and the Fertile Crescent contains two Vavilov centres

(Vavilov, 1926). Willcox (2012) stated that early farming started in Southwest Asia (the Fertile Crescent today). Willcox (2012) also specified that nine major crops were domesticated in this region including einkorn, emmer, barley, lentil, pea, chickpea, bitter vetch, broad bean, and flax (Willcox 2012).

It was estimated that 390,900 vascular plants are known to humans (Kew, 2016). The number of vascular plants in Turkey is 9,753 taxa (Guner et al., 2012).

Figure 2-1. A map showing the location of the Fertile Crescent countries created using ArcGIS Pro 2.4.

In Syria, vascular plants amounted to 3,500 plants (Post, 1933). Zohary (1966, 1986) illustrates that the number of vascular plants in Israel and Palestine is 2,700 taxa. Taifour and El-Oqlah (2017) recently updated the vascular plants list in Jordan and now it is 2,600 taxa (Taifour and El-Oqlah, 2017). Lebanon has 2,606 vascular plants (Mouterde 1970). Iraq has 3,220 vascular plants (Ghazanfar and McDaniel, 2015). The number of vascular plants in the Fertile Crescent equals 21,080 species

(Ghazanfar and McDaniel, 2015). Vincent et al. (2013) state that the Fertile Crescent is one of the regions with the highest concentration of CWR per unit area globally. Lebanon, Israel, Greece, Portugal, Azerbaijan, Bulgaria, Syria, Italy, Spain, and Turkey are areas with the top CWR concentration per unit, four of them found in the Fertile Crescent (Lebanon, Israel, Syria, and Turkey) (Vincent et al., 2013). Castaneda-Alvarez et al. (2016) also emphasised that the Mediterranean is one of the richest regions in the world for CWR, with 84 global priority taxa in every 25 km^2. Such findings confirm that the Fertile Crescent, as part of the Mediterranean basin, is a hotspot for crop diversity (Castaneda-Alvarez et al., 2016). The Fertile Crescent is possibly the most important centre for ensuring global food security, yet a number of studies that have been undertaken on CWR genetic erosion in the region (Keisa et al., 2008) indicate that local CWR diversity is being rapidly eroded. Combined with the likely adverse impact of climate change, there is a need to apply contemporary genetic and GIS techniques as an aid to the development of a regional CWR conservation strategy for the Fertile Crescent to help in safeguarding global food security. This paper addresses the creation of a CWR checklist, prioritisation, and the creation of a CWR inventory as a first step towards developing a CWR conservation and use strategy for the region.

2.4. METHODS

To create the CWR checklist, the PGR forum was used. This is an online database designed to facilitate CWR conservation and CWR use for Euro-Mediterranean countries. The catalogue was built with a set of available databases including Euro Med PlantBase (http://www.euromed.org.uk/), Mansfeld's World Database of Agricultural and Horticultural Crops (Hanelt and IPK, 2001; http://Mansfeld.ipk-gatersleben.de/Mansfeld/), with forestry genera from the enumeration of cultivated forest plant species (Schultze-Motel, 1966), and ornamental genera from the Community Plant Variety Office (http://cpvo.europa.eu/en) and Schippmann et al. (2002) (Maxted et al., 2007). Cwrdiversity was also used; this is an online database for information on CWR (Vincent et al., 2012) (http://www.cwrdiversity.org).

Table 2.1. Groups for the production value (in 1,000 USD)

Group	Range (in 1000 USD)	Points
G0	Below 1	0
G1	1–2,554	1
G2	4,765–27,146	2
G3	27,170–52,983	3
G4	54,696–103,121	4
G5	105,340–149,290	5
G6	164,134–235,667	6
G7	236,222–378,381	7
G8	392,493–668,148	8
G9	689,250–3,951,780	9
G10	4,903,859	10

The regional plant checklist consists of a widely accessible working set of known plant species with accepted Latin names. The introduced plant species were excluded, but the near-endemic species were included in order to obtain a complete and comprehensive regional species checklist of the native species. The checklist went through thorough evaluation as there were lots of duplications and synonyms. Species names were checked thoroughly against many sources. The work of Mansfeld, Zeven and de Wet (1982) was used to get a more comprehensive list. After checklist approval, prioritisation started. The regional plant checklist was prioritised following several criteria comprising production value, projected production value, production area (ha), projected production area (ha), native status, energy supply (kcal/capita/day), protein supply (g/capita/day), fat supply (g/capita/day), occurrence status, gene pool, taxon group, and threat status.

Table 2.2. Selection criteria, groups, and point scale used for the prioritisation.

Criteria/Group	**Points**										
	0	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
Production Value (MXP)*[1]	G0	G1**	G2	G3	G4	G5	G6	G7	G8	G9	G10
Projected Production Value (MXP)*[2]	G0	G1**	G2	G3	G4	G5	G6	G7	G8	G9	G10
Production Area (has)*[1]	G0	G1**	G2	G3	G4	G5	G6	G7	G8	G9	G10
Projected Production Area (has)*[2]	G0	G1**	G2	G3	G4	G5	G6	G7	G8	G9	G10
Native Status*		Non-nat									Nat
Energy Supply (kcal/capita/day)*[3]	G0	G1**	G2	G3	G4	G5	G6	G7	G8	G9	G10
Protein Supply (g/capita/day)*[3]	G0	G1			G2				G3		
Fat Supply (g/capita/day)*[3]	G0	G1			G2				G3		

Occurrence Status[4]	Inv				Int						Nat
Gene Pool Level[5]		GP3				GP2					GP1
Taxon Group Level[6]		TG4			TG3			TG2			TG1
Threat Status IUCN[7]	LC	LC	LC	LC	LC	NC	VU	EN	EN	CR	CR

* Values of the related crop; ** G0–G10: categories for the corresponding criterion values (Int $1,000) from to 2014.

Inv invasive, *Int* introduced, *Nat* native, *GP* gene pool, *TG* taxon group, *LC* least concerned, *NT* near threatened, *VU* vulnerable, *EN* endangered, *CR* critically endangered

The production value of crops was taken from FAOSTAT (2016), which is a database that shows production for the 20 most important agricultural commodities for each country around the world. FAOSTAT's (2016) database allows users to compare production and yield for certain food crops for several countries. The economic value of crops in the Fertile Crescent has been taken from the CROP-FAOSTAT unit (http://faostat.fao.org/default.aspx?PageID= 567#ancor). As shown in Table 2.1, points were allocated to CWR according to their production value (in 1,000 USD).

The CWR species are ranked from closely related to more remote ones as follows: primary gene pool (GP1), secondary gene pool (GP2), and tertiary gene pool (GP3). The database was accessed to check the gene pools of CWR species that occur in the Fertile Crescent. The International Union for Conservation of Nature (IUCN) (http://www.iucnredlist.org/) has notable information aimed at assessing the risk of extinction to species. The IUCN Red List is designed and managed by the IUCN Global Species Programme and the Species Survival Commission (SSC). It is established upon specific criteria to assist in knowledge of the conservation status of species globally. Selection criteria, groups, and point scale used for the prioritisation are summarised in Table 2.2.

A simple ranking system (SRS) was used and each CWR was given a score accordingly. Each group is allocated a number of points based on the importance or implication of the level/status of the group. For example, invasive taxa get 0 point and native get points; introduced get 4 points. The number and range of the categories are from G0 to G10 and are determined according to the occurrence status. Ten groups were created and linked to the production value (from G0 to G10). G0 means the CWR has no commercial value at all and G10 has 10 points. The higher the production value of the crop, the more points it scores. Ten groups were established to represent the production value (Table 2.2); each category gets a number of points. In this case the larger the production value, the more points the taxa get. Once the points were allocated to all the groups for each criterion, the next step was to apply these methods to each CWR species in the regional checklist and relate the matching points. The final points for species are the total score of all the criteria listed. Species that got the highest score are the top priority; then the inventory was formed of the first 220 species on the list. The inventory was sent to ICARDA for approval as the ICARDA is one of the leading centres in conserving plant genetic diversity in the region. The species in the inventory were evaluated and confirmed that they represent the most important CWR in the region.

2.5. RESULTS

The total number of taxa in the Fertile Crescent is 21,080 taxa and 835 taxa are CWR that are related to crops which have socio-economic value in the region.

The 835 taxa of the Fertile Crescent went through prioritisation processes. The first 220 species based on the twelve prioritisation criteria. The remaining 615 are excluded from the list as they are of lower priority. The CWR priority list contains CWR taxa and relates to cereal, vegetable, and industrial crops and 35 taxa relate to fruits and trees. Figure 2.2 shows the organisation of the taxa in the CWR checklist and the CWR inventory.

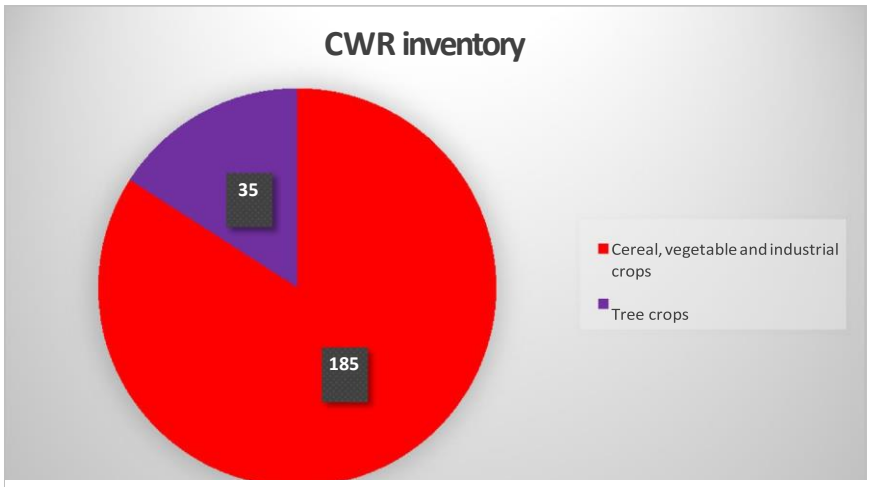

Figure 2-2. The organisation of the taxa in the CWR checklist and the CWR inventory

CWR related to cereals, vegetables and industrial crops accounted for 84% of the CWR inventory. CWR related to trees accounted for 16% of the CWR inventory (Figure 2.3).

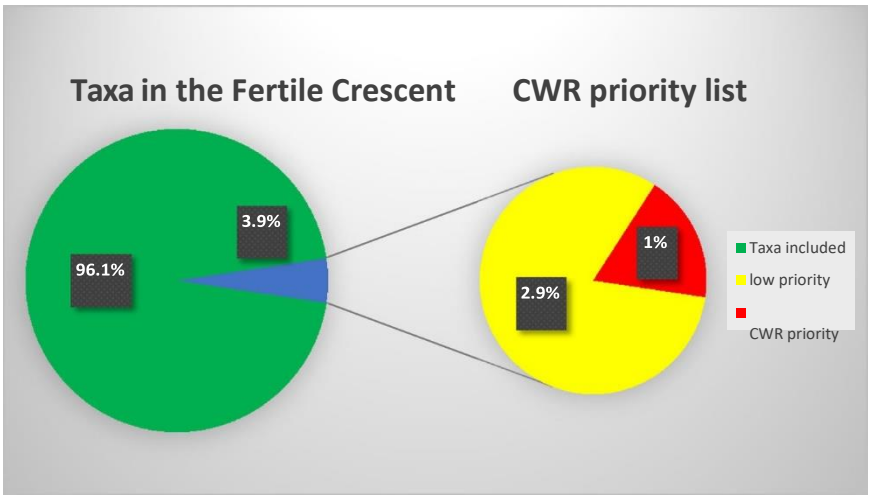

Figure 2-3. CWR inventory

Figure 2.4 shows the number of taxa per genus included in the priority list.

Figure 2.5 shows the number of CWR taxa per genus listed in the tree wild relatives' priority list.

Table 2.3 represents the number of families, genera, and taxa per general crop use for the CWR included in the inventory.

2.6. DISCUSSION

The purpose of this study is to enhance the conservation of CWR in the Fertile Crescent by creating a CWR checklist for the region, setting prioritisation methods,

and creating a CWR inventory. They are acceptable results as the number of CWR taxa in the checklist is consistent with the number of taxa in the countries of the Fertile Crescent proposed by Ghazanfar and McDaniel (2015). The approach used in prioritisation, which is a species-based method, followed a similar approach as Maxted et al. (1997), Magos Brehm et al. (2010), Khoury et al. (2013) and Fielder et al. (2015), where the focus was on species rather than habitat-based prioritisation. The knowledge generated will enable policy makers to implement effective protocols for conservation and sustainable management of such critical plant genetic resources. CWRs play an essential role in the current and upcoming food security strategies; they are a potential source of diversity for domesticated species. CWRs have contributed to improved cultivation by introducing resistant genes against many insect and plant diseases. In addition, they provide improved tolerance to salinity, drought, and extreme temperatures. There is a broad diversity of crops and their wild relatives throughout the Fertile Crescent. For the above-mentioned reasons, this study aims to analyse the diversity of wild relatives of the most significant crops in the Fertile Crescent as a keystone for implementing a regional conservation strategy for such genetic resources. The study will help generate and apply a CWR conservation strategy for the region. Recommendations for further research is to undertake a gap analysis and to generate and apply a CWR conservation strategy for the region. This will help the world stand against climate change and other threats to agriculture biodiversity and food security. The results and conclusions of this study are important as it is the first time somebody has created a CWR checklist and prioritised and created a CWR inventory for the Fertile Crescent. These three elements are the first step toward conservation of genetic resources to help our planet stand against climate change and other threats to agriculture biodiversity and food security.

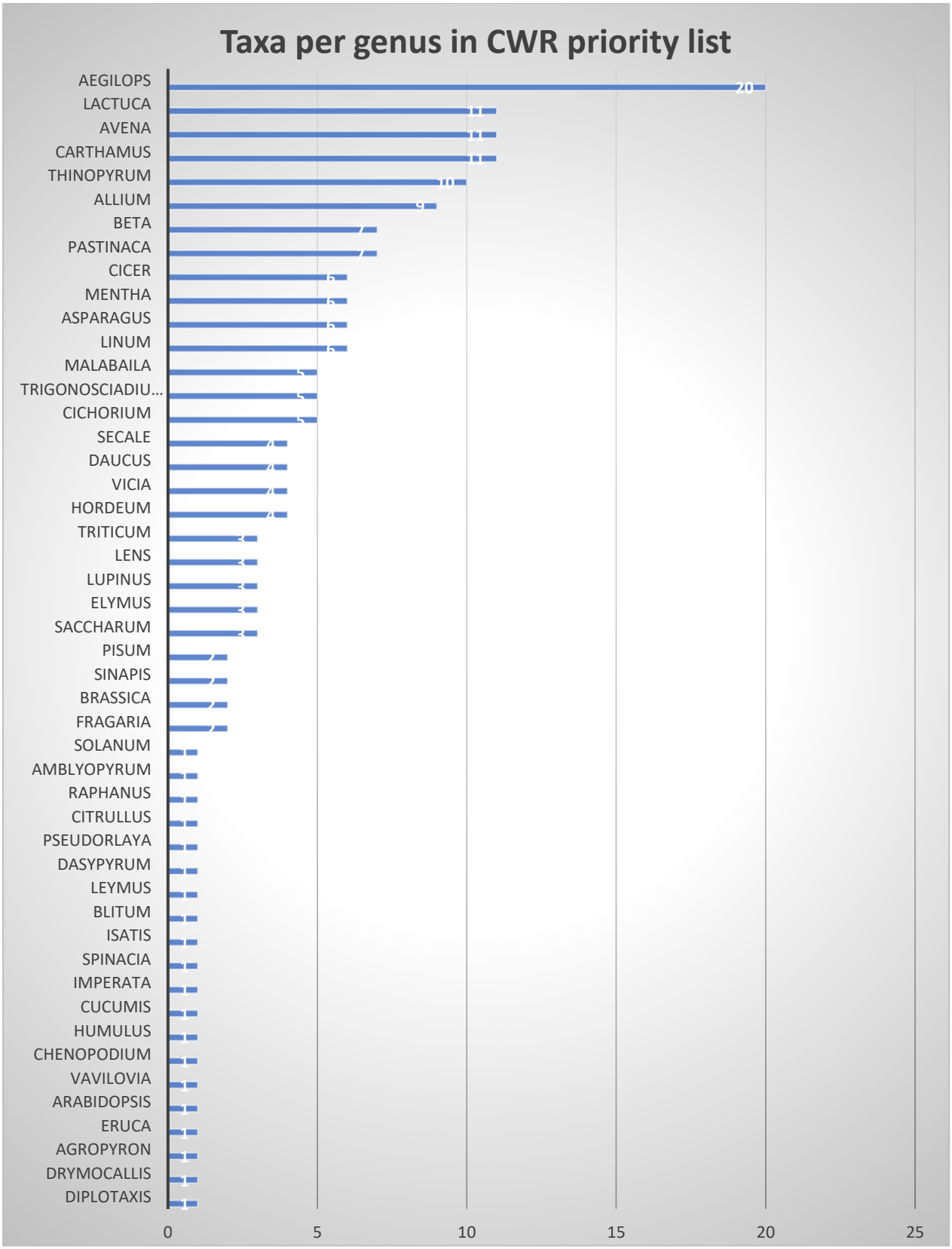

Figure 2.4 shows the number of taxa per genus included in the priority list.

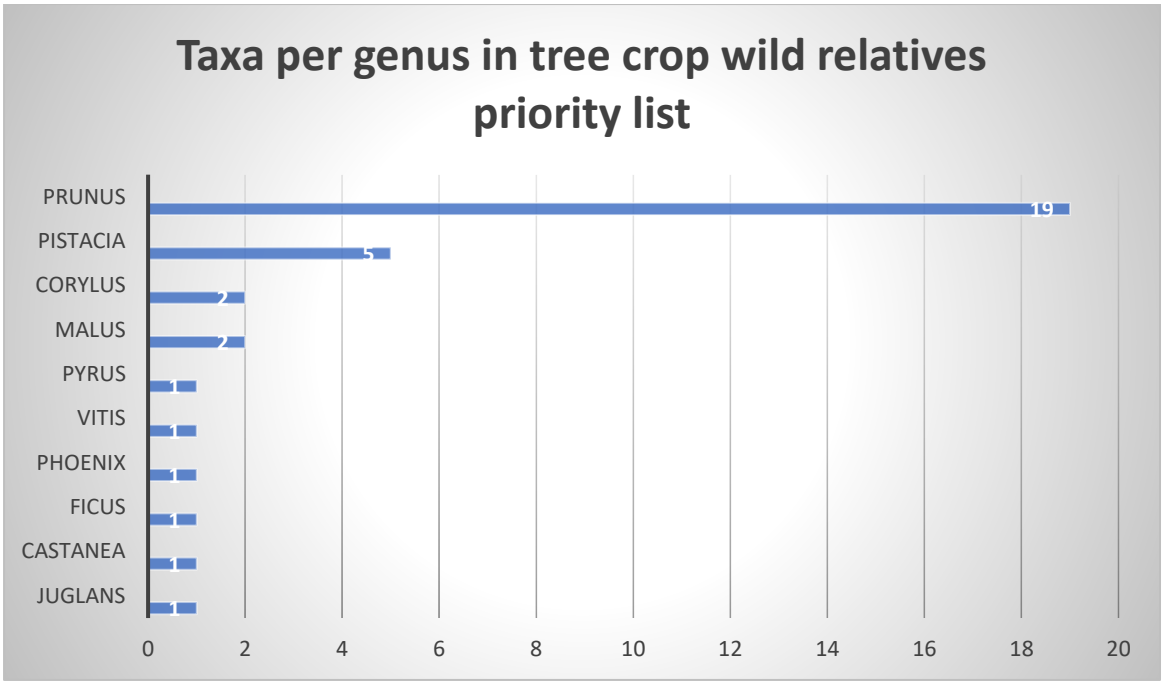

Figure 2-5. Number of CWR taxa per genus listed in the tree wild relatives' priority list.

Table 2.3. Number of families, genera, and taxa per general crop use for the CWR included in the inventory

	Priority list	
General Crop Use	**Families**	**Genera**
Cereal	2	6
Forage	1	3
Fruit and nuts	8	18
Industrial	2	3
Legume	1	5
Herb and spice	2	2
Oilseed	2	2
Vegetable	8	15
Total	26	54

2.7. CONCLUSION

We present the first inventory of 220 priority CWR for the Fertile Crescent. The inventory helps to improve the *in-situ* and *ex-situ* conservation and the genetic diversity of CWR. Both the inventory and the methodology applied in prioritisation are applicable and can be used in setting national, regional, and global conservation strategies. The recommendations will help the Fertile Crescent meet its targets in conserving CWR diversity as well as making sure that CWR genetic resources are preserved to prevent and tackle global food insecurity.

3. CHAPTER 3: *EX-SITU* AND *IN-SITU* CONSERVATION GAP ANALYSIS OF CROP WILD RELATIVE DIVERSITY IN THE FERTILE CRESCENT OF THE MIDDLE EAST

3.1. AUTHORS AND AFFILIATIONS

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3.2. ABSTRACT

Crop wild relatives (CWR) are important reservoirs of adaptive traits for crop breeding programmes. Both *ex-situ* and *in-situ* conservation approaches should be deployed to ensure their availability for use. The purposes of this paper are: a) to create a regional database of occurrence records for the 441 priority CWR in the Fertile Crescent; b) to find CWR-rich areas in the Fertile Crescent; c) to recommend locations to implement genetic reserves intended for active *in-situ* conservation of CWR; and d) to undertake *ex-situ* and *in-situ* conservation gap analysis following different methods, one using Maxent and Diva GIS and one using CAPFITOGEN. The study area comprises Jordan, Syria, Palestine/Israel, Lebanon, Turkey and Iraq. Occurrence records of the Fertile Crescent CWR priority list were gathered from herbaria, gene banks and online databases. Hotspots of CWR diversity were obtained and complementarity analysis was carried out in order to identify areas for active *in-situ* conservation using DIVA-GIS. Gaps in *in-situ* and *ex-situ* conservation were identified using both MaxEnt and DIVA-GIS. Proposed genetic reserves for CWR were compared to existing protected areas in the *in-situ* gap analysis. Gaps in the representation of priority CWR in gene banks were identified in the *ex-situ* gap analysis. A total of 23,878 occurrence records were collated for 441 CWR priorities. The first priority grid square is located in Syria near Tal Kalakh City, close to the Lebanese border from the north. The second priority site is located in Turkey in Izmir Province near Kemal Atatürk Mahallesi. The third

priority site is located in Turkey in Sahinbey/Gaziantep Province. The *ex-situ* gap analysis revealed that only 70% of the CWR examined taxa are represented in gene banks. The most important areas for further collecting for *ex-situ* conservation are located in the west and south of Turkey across the Mediterranean seashore, North Lebanon and west of Syria (in Lattakia and Tartus Governorate), across the border between Turkey and Syria and northern Iraq. Ten genetic reserves are recommended in the Fertile Crescent for CWR conservation. A complementarity analysis using CAPFITOGEN VERSION 2.0 has been conducted and it was found that the top sites with the highest CWR taxa concentration are found in eastern Turkey, with two blue grid squares containing at least 36 CWR taxa each. The next highest CWR taxa is found in north-east turkey, not far from the first two. The fourth highest CWR taxa is found in Latakia in Syria with the light blue square containing 20-35 CWR taxa. The fives, sixth, seventh highest CWR taxa are found in Turkey with the yellow square containing 9-20 CWR taxa, one in Izmir Province, one in Kumluca Antalya, and one in the South-eastern Anatolia Region. There are several priority squares with the orange colour containing 5-9 CWR taxa. The first one is in the Zabadani District in Syria and the rest are in Turkey. It was noticed that Jordan does not have any grid squares and in Iraq, there is only one red grid square containing 1-5 CWR taxa. The results and methods used will help in meeting the conservation targets for CWR in the Fertile Crescent and will be an aid to achieving global food security.

3.3. KEYWORDS

Conservation, gap analysis, species richness, complementary analysis, genetic diversity.

3.4. INTRODUCTION

The Fertile Crescent is a geographical term that has been used historically to describe the northern part of the Middle East and the eastern coast of the Mediterranean Sea from Jordan, Syria, Palestine/Israel, Lebanon and Turkey, to Iraq (Breasted, 1916; Clay, 1924). It is recognised not just for plant species concentration but specifically for its agrobiodiversity wealth (Vavilov, 1926; Zhukovsky, 1950; Harlan, 1951; Harlan and Zohary, 1966; Zohary, 1969), both in terms of its rich diversity of cultivated plants and diversity of their wild relatives. It is the centre of domestication for major crops such as *Triticum monococcum* (einkorn wheat), *Triticum durum* (durum wheat), *Triticum*

turgidum (poulard wheat), *Triticum aestivum* (bread wheat), *Hordeum vulgare* (cultivated two-rowed barley), *Secale cereale* (rye), *Avena byzantina* (red oat), *Cicer arietinum* (chickpea), *Lens esculenta* (lentil), *Pisum sativum* (pea), *Medicago sativa* (blue alfalfa) and *Sesamum indicum* (sesame) (Hawkes, 1983; Morrell, 2007). The Fertile Crescent region has significant historical value as agriculture was first developed there and recent evidence indicates that agriculture started on a small scale in Ohalo II in Israel around 23,000 years ago (Snir, 2015).

There is an increasing demand for this agrobiodiversity to help produce more food to feed an increasing human population, which is expected to reach 11.2 billion by 2100 (UN, 2017), and there is an increase in customers' expectations to produce quality crops. The lack of natural resources such as water and farming land, climate change and pollution of land and water have put further pressure on food and agricultural production globally (FAO, 2011; Asseng *et al.*, 2015). Although agricultural demand can be met in part by reducing food wastage (Tilman and Clark, 2014), increased agricultural production is needed and should be sustainable (Godfray *et al.*, 2010). To achieve global food security, 90% of the increase in food production will have to come from intensive agriculture and increased crop yield (FAO, 2009). One of the major contributors to increased agricultural production is to improve crop varieties using novel genes donated from CWR by not only improving tolerance to different climate conditions and resistance to pests and diseases, but also by improving yields (Maxted *et al.*, 2000; Araus *et al.*, 2008).

CWR are wild plants closely related to crops and therefore important sources of novel traits (Maxted *et al.*, 2006) because they possess the greatest breadth of adaptive trait diversity as they have not passed through the domestication bottleneck (Tanksley and McCouch, 1997). One element complementary to reaching food security is to conserve *in situ* and *ex situ* and use CWR in crop breeding programmes (Maxted *et al.*, 1997; Zhang *et al.*, 2017). The need to increase food production in the face of climate change necessitates increased use of CWR diversity to provide the required trait diversity (Maxted *et al.*, 2012; FAO, 2015), especially in the Fertile Crescent context where increasing drought has been recorded as a result of climate change (Kelley *et al.*, 2015). Vincent *et al.* (2013) established and Castaneda-Alvarez *et al.* (2016) confirmed this region as the global centre of CWR concentration with 84

global priority taxa per 25 km^2; therefore, conserving the region's CWR diversity is vital for global as well as regional and local national food security.

Assessments performed by Castaneda-Alvarez *et al.* (2016) revealed that a third of CWR had no accessions and 72% were a high priority for collection. Furthermore, CWR are threatened in their natural habitats due to urbanisation, climate change, and land and water pollution (Jarvis *et al.*, 2008). Kell *et al.* (2012), using the IUCN Red List threat assessment methodology, found that 16% of European CWR are threatened with extinction. In the Fertile Crescent, CWR are specifically threatened by the construction of buildings, infrastructure, roads and railways, as well as overgrazing and climate change (El-Beltagy, 2006; Derneg, 2010; Trigo *et al.*, 2010).

Gap analysis is now routinely used as a tool for agrobiodiversity conservation planning (Maxted *et al.*, 2013). It involves finding gaps in existing conservation actions and identifying the under-represented elements, therefore helping to prioritise additional actions (Scott, 1993). In the CWR context, it involves comparing the range of natural diversity to the diversity already conserved *ex situ* in gene banks or *in situ* in genetic reserves. The gaps become the recommended additional conservation actions (Magos Brehm *et al.,* 2017).

The objectives of this study are to facilitate the conservation of CWR by conducting a gap analysis of 441 priority CWR related to 61 crops and recommend actions to conserve their gene pool more effectively to make their genetic material available for farmers' and breeders' utilisation.

3.5. METHODS

Occurrence records were collated for the priority list of 441 CWR taxa in the Fertile Crescent from herbaria, gene banks, and online databases (Zair *et al.*, 2017). The occurrence data was not collated in the Zair *et al.* (2017) reference. Although the arc of the Fertile Crescent comprises only parts of Iraq, Israel, Jordan, Lebanon, Palestinian Territory, Syria and Turkey, the conservation gap analysis was conducted for the entire countries. Where records had no geographic coordinates but had specific locations, latitudes and longitudes were obtained using the GEOLocate (2017) software. Occurrence data were then verified, and those that occurred outside the boundaries of the Fertile Crescent or found in the sea were either corrected or deleted (Scheldeman and van Zonneveld, 2010). The occurrence records were then plotted

using DIVA-GIS Version 7.5 (Figure 3.1). A species richness map was also plotted using DIVA-GIS Version 7.5 with a grid cell of 0.2 degrees (~22.2 km^2) by applying the 'Point to Grid' and 'Richness' tool (Scheldeman and van Zonneveld, 2010). CWR observation richness was plotted using DIVA-GIS Version 7.5 with a grid cell of five minutes (~9 km^2), and a complementarity analysis was plotted using the 'Point to Grid' and 'Reserve Selection' functions in DIVA-GIS Version 7.5 using a cell size of 0.2 degrees and applying the Rebelo *et al.* (1994) algorithm. Figure 3.2 demonstrates the observation richness of CWR priority taxa. The map indicates northwest Syria and northern Lebanon as regions with the highest concentration of CWR. Figure 3.3 shows the complementarity analysis of priority CWR sites and existing protected areas in the Fertile Crescent. Proposed *in-situ* reserve locations were compared to existing locations of protected areas. Existing layers of protected areas were taken from the Protected Planet (2018) database. An analysis to cover two thirds of the CWR taxa has been undertaken. The top two thirds of the total 441 CWR equal 294 CWR taxa (441X2/3=294). CWR taxa for each site were added until reaching 294 or more.

CWR taxa to cover 2/3 of the CWR =S1+S2+S3+S4

S1 number of CWR taxa in site 1

S2 number of CWR taxa in site 2

S3 number of CWR taxa in site 3

S4 number of CWR taxa in site 4

For the *ex-situ* gap analysis, gaps in the ecogeographic representation of CWR priorities of the Fertile Crescent in gene banks were identified (Figure 3.4, Supplementary Tables 1 and 2) following the methodology suggested by Ramirez-Villegas *et al.* (2010) and followed by Castaneda-Alvarez *et al.* (2016). Species distribution models for the 441 taxa were obtained using MaxEnt Version 3.4 (Phillips *et al.*, 2006). The 19 bioclimatic variables extracted from WorldClim (Fick and Hijmans, 2017) and outlined in Supplementary Table 3 were used in the models. A total of 10,000 random points was used as background records across the study area and fivefold cross-validation (k=5) was implemented. Maximum training sensitivity and specificity thresholds were used to restrict the modelled potential distributions.

Only models that fulfilled the following validation criteria were considered stable and used in further analyses (Ramiréz-Villegas *et al.*, 2010):

- Fivefold average area under the test data ROC curve (ATAUC) above 0.7.
- Standard deviation of ATAUC (STAUC) below 0.15.
- Proportion of potential distribution area with standard deviation above 0.15 (ASD15) below 10%.

For those taxa that lacked stable models, a 50 km round buffer was applied when only ten present points are available. In order to assess whether the species conserved *ex situ* was ecogeographically and adequately conserved, three scores were estimated: the Ramiréz-Villegas *et al.* (2010) geographic representativeness score (GRS), the environmental representativeness score (ERS), and the sampling representativeness score (SRS). In order to prioritise each target taxon for collecting for *ex situ* conservation, all representativeness scores (SRS, GRS and ERS) were averaged with an equal weight to obtain the final prioritisation score (Ramiréz-Villegas *et al.*, 2010). As adopted from Castaneda-Alvarez *et al.* (2016), if the Final Priority Score (FPS) is more than seven, the taxon is considered of high priority for *ex-situ* conservation, if the score is between five and seven, the taxon is considered of medium priority and if between 2.5 and 5, the taxon is considered of low priority for conservation. Geophysical and bioclimatic variables were standardised in Excel and tested for collinearity (Dormann *et al.*, 2013) by running an R script (see Appendix) which resulted in 11 variables composed of all five geophysical variables and six bioclimatic variables (bio_15, bio_3, bio_5, bio_6, bio_8 and prec_6). The five geophysical and six bioclimatic variables were then run through a principal component analysis (PCA) in SPSS, where variables were chosen based on the highest loadings (>0.3). This resulted in four geophysical variables (slope, altitude, northness and eastness) and three bioclimatic variables (bio_8, bio_6 and bio _15). CWR potential richness was calculated in MaxEnt Version 3.4. The result of MaxEnt was uploaded to DIVA-GIS Version 7.5. The DIVA-GIS result is displayed in Figure 3.5. The Figure 3.6 map resulted from overlaying the potential richness map with the current route richness diversity layer. The aim of the Figure 3.6 analysis is to find gaps for further collections. In summary, this analysis aims to find projected hotspots for future collection of high-priority CWR. Plant genetic materials from these projected hotspots can be used in

ex-situ conservation and gene banks. Another method to undertake the gap analysis is by conducting the Ecogeographic Land Characterisation (ELC) analysis in CAPFITOGEN Version 2.0 and applying the ELCmapas tool (Parra-Quijano et al., 2014). The gap analysis using CAPFITOGEN VERSION 2.0 has been conducted for the Fertile Crescent in this study. The occurrence dataset using the CAPFITOGEN VERSION 2.0 passport format has been created. Quality check was performed on the data by running it into CAPFITOGEN VERSION 2.0. The data were reanalysed again to not miss any genus name. A total of 30396 occurrence records were inserted manually in the CAPFITOGEN VERSION 2.0 passport format sheet. There were rules for each column, as an example, the collection date should be inserted in below format for every single species YYYYMMDD. The type of the complementarity analysis was run is complementarity based on grids but also on existing protected areas. The source of protected areas layers is ProtectedPlanet.net (2019). The original data has other countries included (not only the Fertile Crescent), so these have been eliminated one by one and only countries in the Fertile Crescent remained. Revised dataset for the Fertile Crescent has been established. Collating the data consumed considerable amount of time to make sure the dates are in the format required for this analysis and latitudes and longitudes are all there for both the genus and the species with full digests for all species. The ADM1, ADM2, ADM3 and ADM4 fields have been filled, checked for missing information and corrected. The roads and site indications in the COLLSITE field were relocated. The ADM fields were filled. WDPA maps layers were used in this analysis. It contains two shapefiles representing PA maps from protectedplanet/WDPA, one for the countries with PA well represented and the other for the all the targeted countries. These layers and the BackgroundMaps ones as well are useful to create the background of the figures illustrating complementarity analysis in ArcGIS.

3.6. RESULTS

Crop wild relatives in the Fertile Crescent priority list consist of 441 CWR taxa (Supplementary Table 1). Passport data of these 441 CWR taxa were collated and are presented in Supplementary Table 2. A total of 23,878 presence points (latitudes and longitudes) representing the 441 CWR priority list taxa in the Fertile Crescent are presented in Supplementary Table 3 and used in subsequent analyses. *Hordeum*

vulgare L. subsp*. spontaneum* (K. Koch) Thell*,* a wild relative of barley, had the largest number of presence points with 2,190 occurrence records. *Vavilovia formosa* (Steven) Fed. was found to be the rarest, having only one presence point. The associated crops of the 441 CWR taxa are summarised in Supplementary Table 4 and used in the following analyses.

Presence points for the 441 priority CWR taxa of the Fertile Crescent region are shown in Figure 3.1, and the arc of the Fertile Crescent is visible in Figure 3.2. Ten sites (Figure 3.3 and Supplementary Table 5) are needed to conserve all 441 priority CWR taxa and the number of taxa in each site is indicated in Table 3.1. Ideally, when implementing *in-situ* conservation of CWR, genetic reserves should be located within existing protected areas to limit the costs associated with the establishment of new conservation areas (Dulloo *et al.*, 2008). However, few of the 10 priority sites are located in or adjacent to existing protected areas because of the lack of protected area coverage in the Middle East, but site 7 Anata is relatively close to Wadi el Qilt Nature Reserve in the Palestine Territories. It is suggested that the borders of these protected areas should be extended to include the locations of CWR.

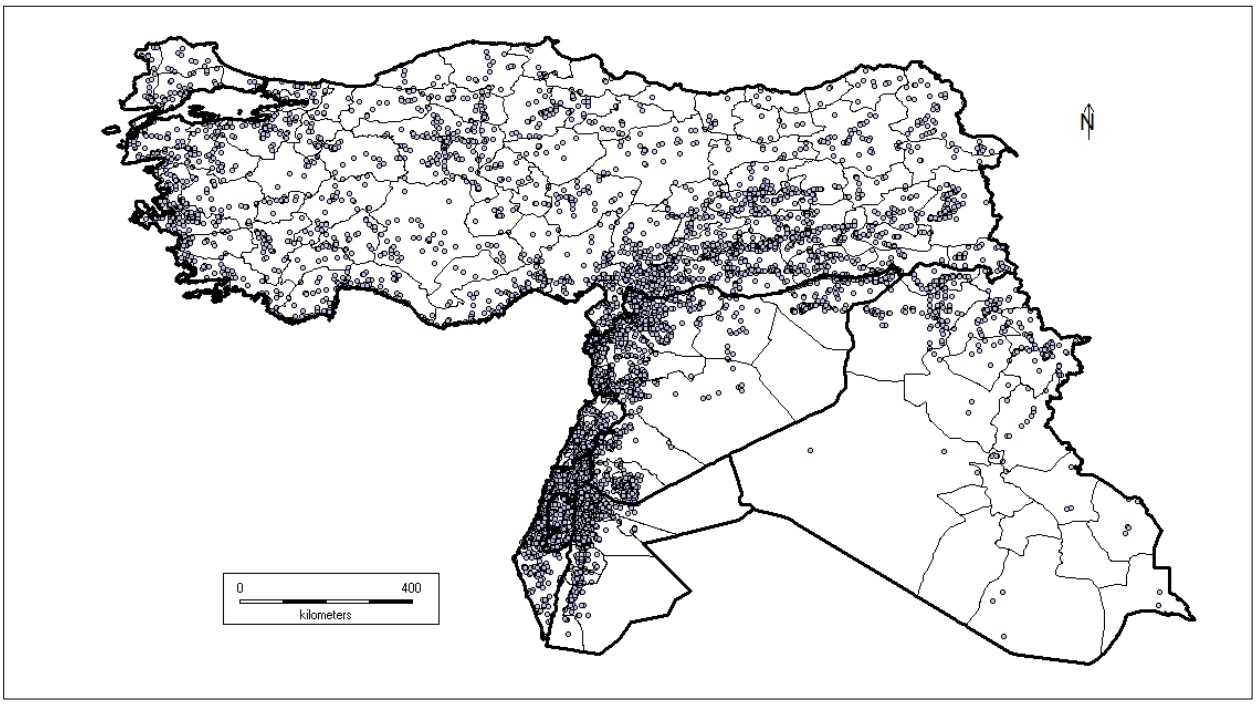

Figure 3-1. Presence points of the 441 priority CWR of the Fertile Crescent

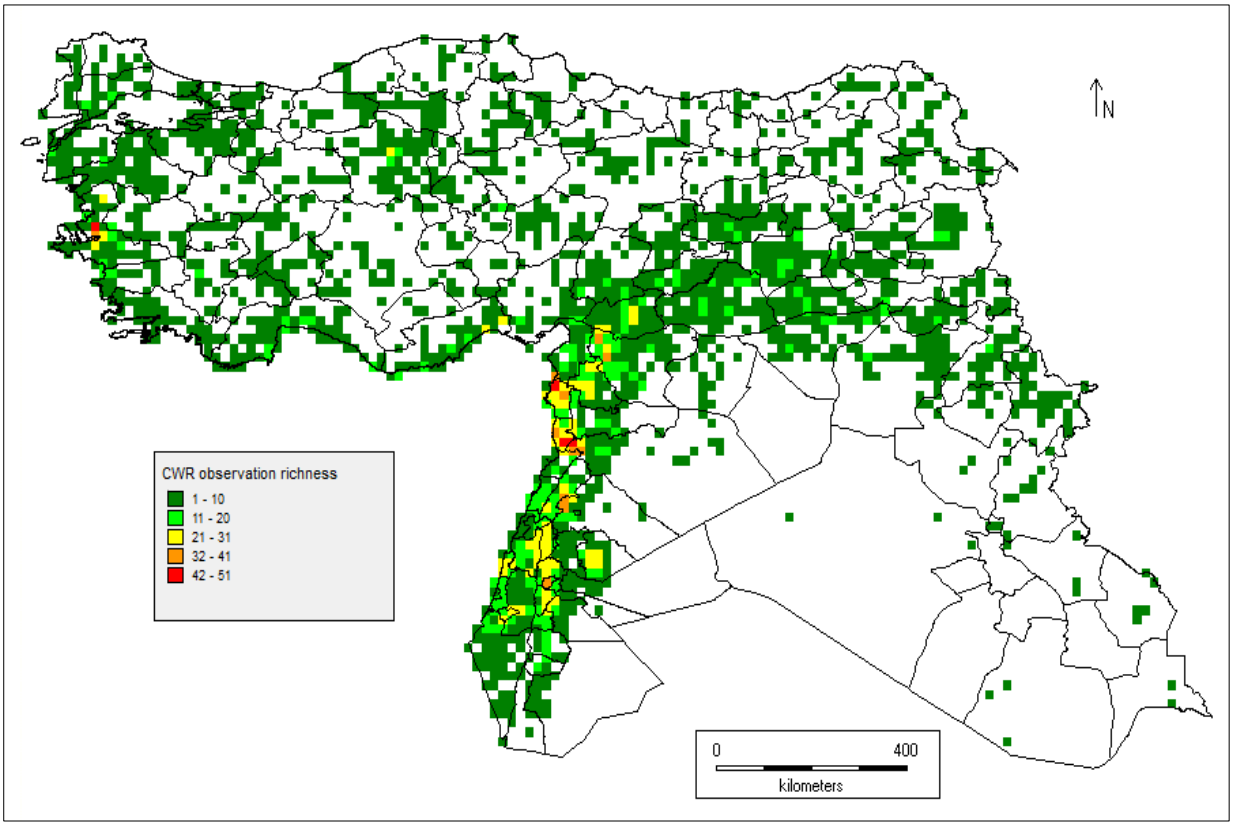

Figure 3-2. CWR observation richness with a grid cell of 5 minutes (~9 km2). Geographic coordinate system is WCS 1984

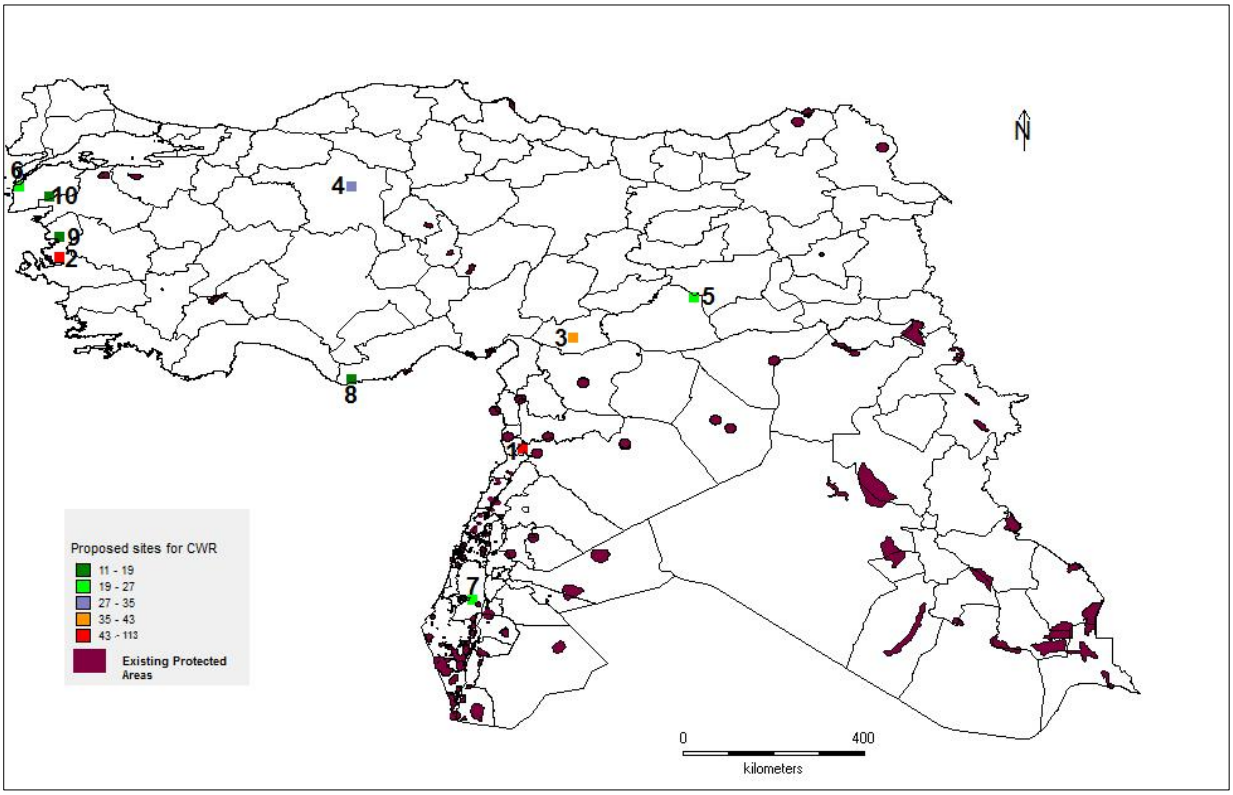

Figure 3-3. Complementarity analysis of 441 priority CWR and existing protected areas in the Fertile Crescent using a cell size of 0.2 degree. All these ten sites cover all 441 CWR taxa.

Table 3.1. Priority sites for in-situ CWR conservation

Site Number	**Country**	**Province**	**Locality**	**Latitude**	**longitude**	**Number of CWR taxa**	**Taxa that do not occur at this site**
1	Syria	Homs	Tel Kalakh	34.730611	36.133611	113	328
2	Turkey	Izmir	Menemen	38.5604	27.0878	112	329
3	Turkey	Gaziantep	Burc Karakuyu	36.9485	37.2360	43	398
4	Turkey	Ankara	Cankaya	39.873040	32.806458	35	406
5	Turkey	Sanlıurfa	Siverek	37.7895	39.6609	27	414
6	Turkey	Canakkale	Kumkale Koyu	39.9735	26.2328	27	414

7	Palestinian Terr.	Jerusalem	Anata	31.8183	35.2596	27	414
8	Turkey	Mersin	Anamur	36.1668	32.8148	19	422
9	Turkey	Edremit	Doyran	39.6730	26.7040	19	422
10	Turkey	Aziziye	Tebrizcik	39.9485	41.0041	19	422
						441 Total CWR taxa	

CWR taxa to cover two thirds of the CWR = S1+S2+S3+S4= 113+112+43+35= 303 CWR taxa. The result found that the first four sites (Homs, Izmir, Gaziantep and Ankara) are needed to cover two thirds of all taxa.

The *ex-situ* gap analysis indicates that priority CWR in the Fertile Crescent (Supplementary Table 6) are under-represented in gene banks. Of the 441 taxa, 134 (30%) CWR are not represented in gene banks at all. Only 307 (70%) CWR are represented in gene banks (Supplementary Table 7), and of these taxa, 252 (57%) have less than 10 accessions in gene banks.

A total of 353 taxa were categorised as a high priority for collection and conservation, 23 taxa as a medium priority and 41 taxa as low priority. However, 24 taxa were identified as not requiring urgent collection (see Supplementary Table 7). The lack of geographical and ecological representation in gene banks lead to high FPS scores, and there are clear gaps in *ex-situ* conservation of these taxa.

As can be seen in Figure 3.4, an examination of CWR taxa sorted by their related crop uncovered that 57 crops (93%) had been relegated to a high need for further gathering and such crops' gene pool requires serious protection activities.

The analysis in Supplementary Table 8 demonstrates that the mean FPS values per related crops are 7.51 for barley, 7.6 for sorghum, 7.88 for oat, 8.17 for pea, 8.95 for sugar beet, 9.59 for rye and 9.63 for sugarcane. The mean FPS values for fruits are 10 for apricot, blueberry, cherry, date palm, peach, persimmon and plum. Four crops (7%) of the crop gene pools had been assigned as a medium priority for further collection, and their FPS values are 6.34 for lentil, 6.1 for wheat, 5.7 for grape and

5.15 for chickpea. As can be seen in Supplementary Table 9, wild relatives of pulses, cereals, oil crops, fruits, industrial crops, sugar crops, herbs, vegetables, nuts, and spices were assessed as a high priority for collection. The mean FPS values for crop types are 8.735 for spices, 8 for pulses, 8.28 for cereals, 8.92 for oil crops, 9.07 for fruits, 9.1 for industrial crops, 9.29 for sugar crops, 9.42 for herbs, 9.47 for vegetables, and 9.575 for nuts.

For all the examined CWR related to 61 crops, no crop gene pool can be considered well represented in gene banks. Wild relatives of wheat have been used as a source of genetic materials for crop improvement and have been collected in gene banks, and they are categorised as a medium priority for collection. Medium priority gene pools such as chickpea and lentil have fewer CWR compared to wheat. As can be seen in Supplementary Table 10 Figure A, the FPS across the CWR priority list in the Fertile Crescent has been categorised according to the gene pool and crop. Although some crops have been assessed as a low priority for conservation, some taxa related to these crops are a high priority for *ex-situ* conservation. Certain CWR related to wheat were evaluated as under-represented in gene banks such as *Aegilops comosa* Sm., *Thinopyrum pycnanthum* (Godr.) Barkworth and *Agropyron cristatum* (L.) Gaertn. Only the high priority category for further collection are presented in Supplementary Table 11. The list of data sources of the occurrence records used in the potential distribution modelling and the gap analysis are summarised in Supplementary Table 12. The environmental variables used in the gap analysis are presented in Supplementary Table 13. A list of experts that evaluated the gap analysis are presented in Supplementary Table 14.

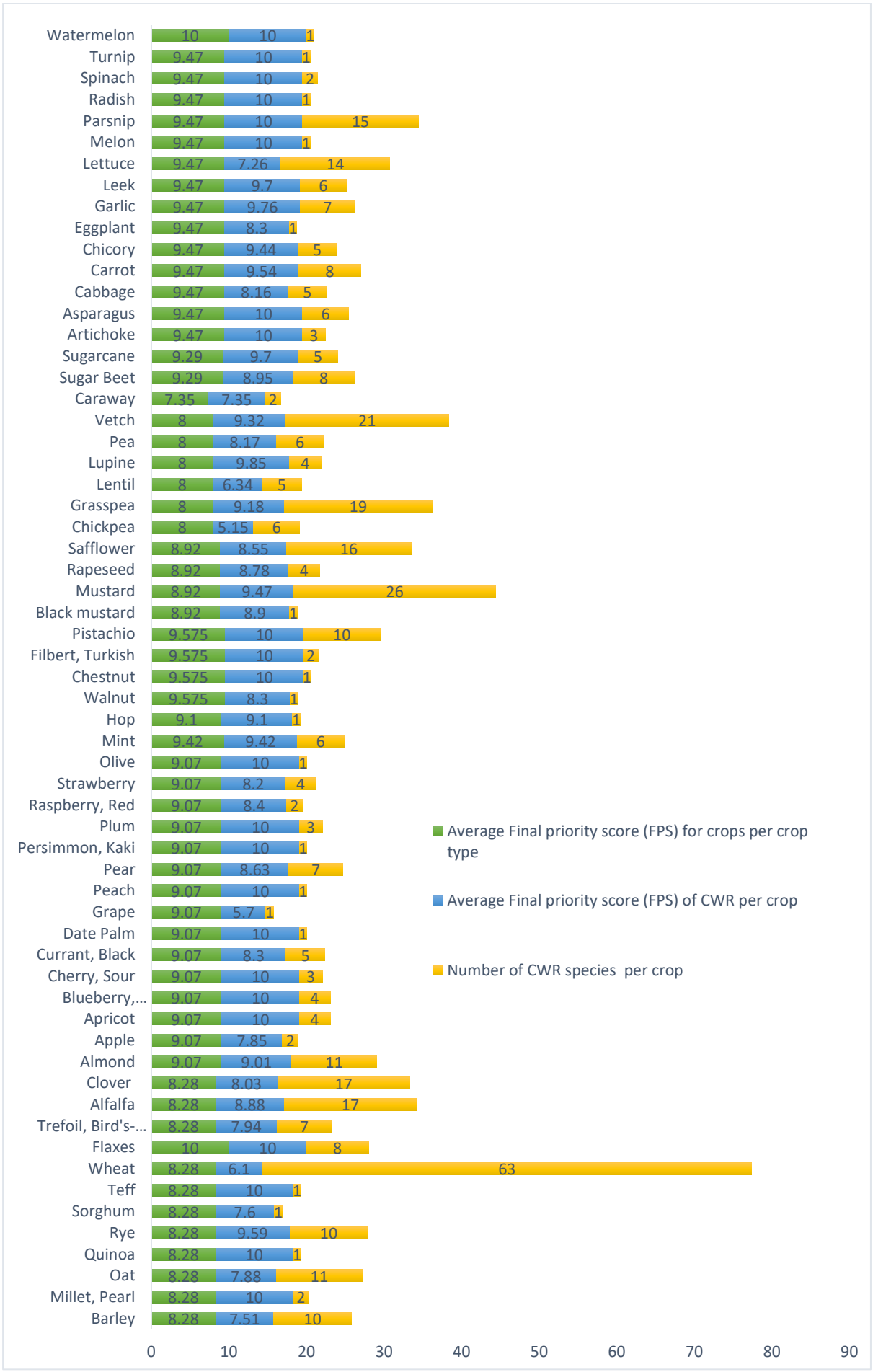

Figure 3-4. Mean priority score values for ex-situ conservation of CWR in the Fertile Crescent.

The gaps in *ex-situ* conservation refer to areas where the taxa potentially occur but accessions for *ex situ* conservation have not been collected and are thus missing in gene banks (Scheldeman *et al*., 2007).

As can be seen in Figure 3.5, the highest concentration of projected CWR diversity is found in the west of Syria, in the area from north Lattakia to south Tartus, alongside the coastal area of Turkey from Bandirma city in the Marmara Sea to Yayladagı town in Hatay province in southern Turkey, across the border between Turkey and Syria and northeast Iraq, across the mountains in Lebanon and seashore, western Jordan alongside the border between Israel and Jordan, and alongside the coastal area of Israel. Some countries, such as Iraq, have few presence points available. However, the analysis revealed that northern Iraq contains high potential CWR taxa richness.

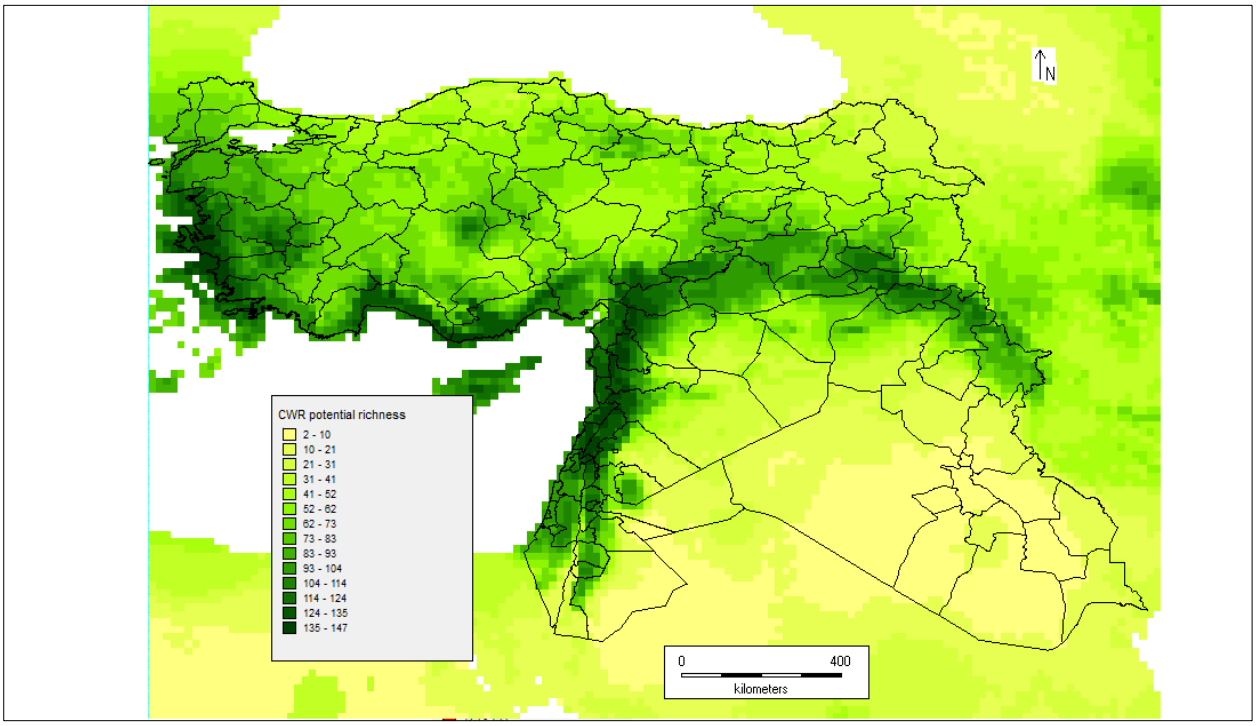

Figure 3-5. CWR potential richness. The legend displays the number of CWR species with a grid cell of 5 minutes (~9 km2).

Ex-situ conservation gaps were identified across the Fertile Crescent regions in Figure 3.6 with the most important gaps found in the west and south of Turkey across the Mediterranean seashore, North Lebanon, the west of Syria in Lattakia and Tartus Governorate, across the border between Turkey and Syria and Northern Iraq. In such

sites, between 133 and 144 CWR taxa are expected to be found in a single grid square.

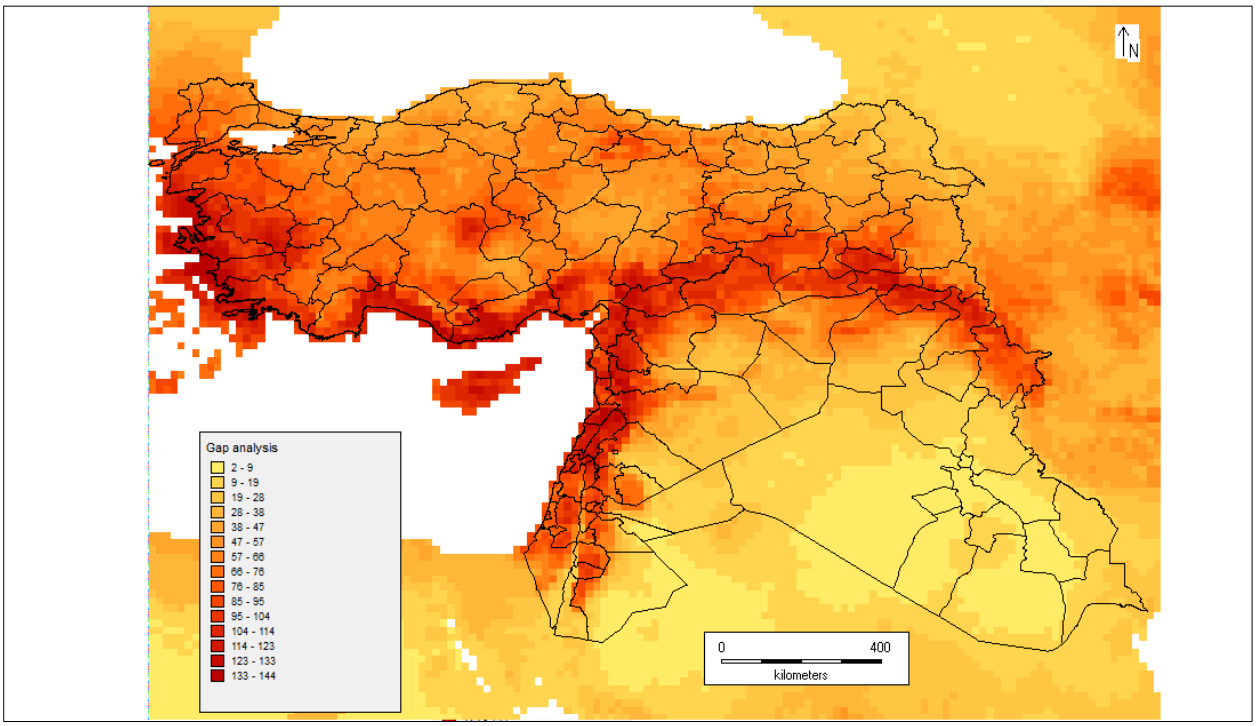

Figure 3-6. CWR ex-situ gap analysis of high-priority CWR in the Fertile Crescent with a grid cell of 5 minutes (~9 km2).

Projected hotspots for future seed collection of priority CWR in the Fertile Crescent are presented. The map corresponds to gaps in *ex-situ* conservation as these taxa are not conserved at all. The legend displays the number of CWR taxa per cell ranging from 133–144. CWR taxa are expected to be found in the extremely dark red of 2–9. CWR taxa per cell in the pale-yellow colour. The map is the result of overlaying the potential richness map with the current route richness diversity layer to find gaps for further collections.

The analysis in Figure 3.6 only considers high-priority CWR taxa. The deep red colour signposts that collection is required in those areas and no *ex-situ* collection has been undertaken before for CWR in these sites, even though these sites are suitable for CWR high priorities. The gap analysis using CAPFITOGEN VERSION 2.0 has been conducted. The CAPFITOGEN VERSION 2.0 passport format sheet has been completed and can be found in supplementary table 15. A total of 0396 occurrence records were inserted manually in this form.

The CAPFITOGEN VERSION 2.0 complementarity analysis result is as follow:

Background maps complementarity analysis contains two shapefiles, one for the countries targeted (Figure 3.7) where it shows PA complementarity analysis for countries with well represented PA maps using ArcGIS Pro 2.4. Figure 3.7 contains the results from Complementa for both cell (5 arc minutes-10 km^2 at the equator cell size) and protected areas analysis. Since it only covers countries with representative PA maps, the PA complementarity and coverage analysis is the most important content. The map shows the orange areas in Al Shouf Cedars Nature Reserve in Lebanon has high concentration of CWR taxa and it is five taxa per grid square. The management of this Reserve should take action to include those CWR in their conservation strategy.

Figure 3.7 also shows CWR presence points exist inside protected areas north of Iraq.

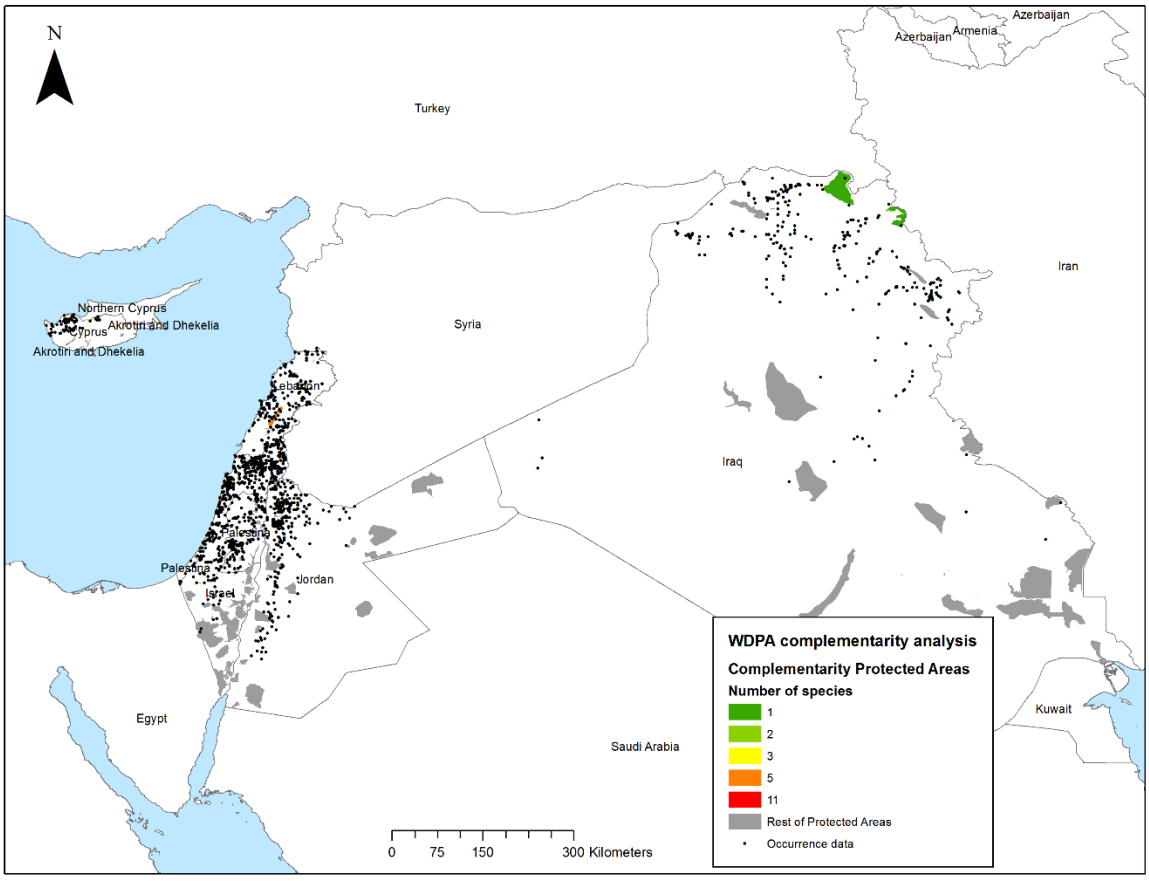

Figure 3-7 shows PA complementarity analysis for countries with well represented PA maps using ArcGIS Pro 2.4.

The other map (Figure 3.8) is for the countries with representative protected areas map (the Fertile Crescent list except Turkey, and Syria). The map is without

occurrences; therefore, it is clearer to see the high priority areas for conservation in north Israel near the border with Lebanon. The number of species is 11 at this area. It is also clearer to see the high priority areas for conservation in North Iraq with the Green colour where the number of CWR species is one. For this and the rest of the complementarity analysis, GEOQUAL info were used to fix a georeferenced quality threshold (TOTALQUAL 100) of 50. without occurrences using ArcGIS .

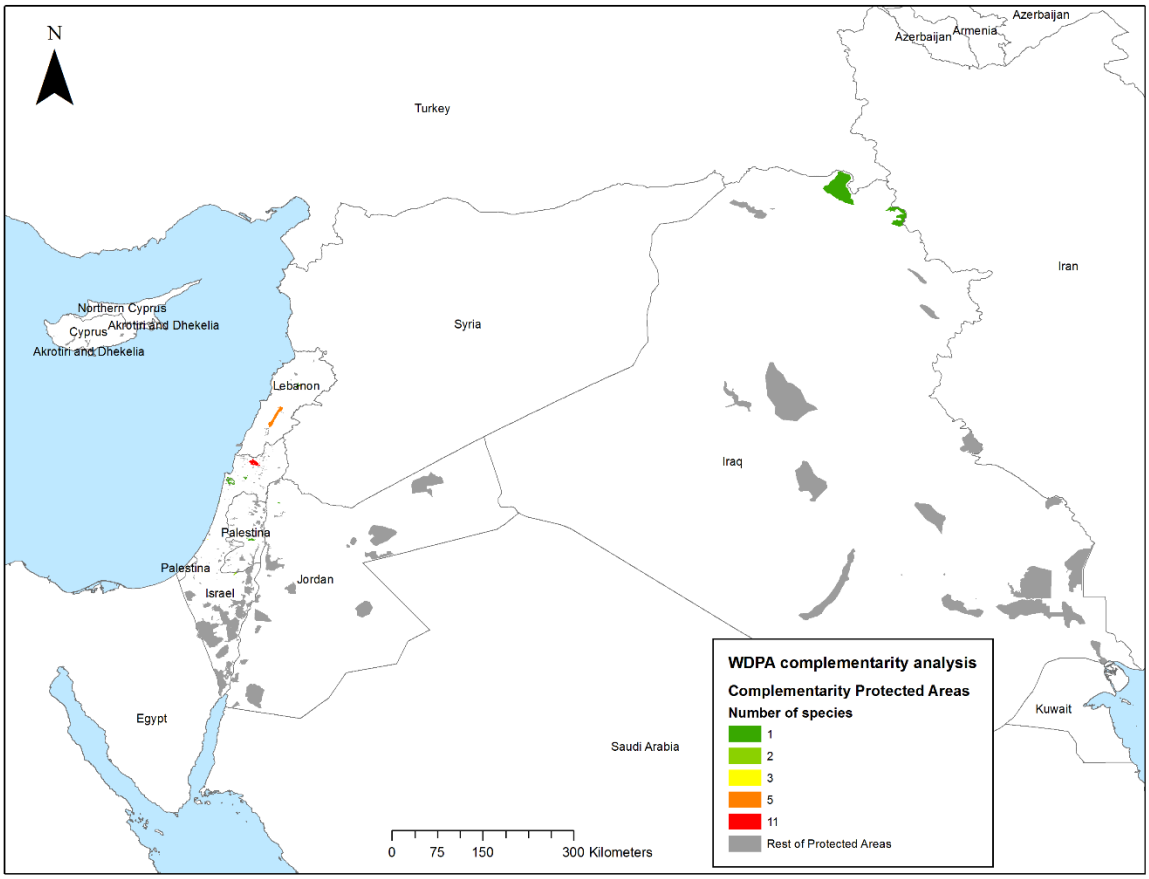

Figure 3-8 shows PA analysis for countries with well represented PA maps without occurrences using ArcGIS Pro 2.4.

In order to project clearer results, a zoom map in some interesting area were produced in Figure 3.9 where there are PA with highest values. The map revealed that areas in Mattat northern Israel has the highest concentration of CWR with 11 in each grid squire. It also revealed that a large area in Jordan next to the Palestinian boarders close to the Dead Sea has high concentration of CWR with three species in each grid squire. It also revealed that an area in Jordan in Yarmouk Nature Reserve has at least one CWR taxa in each grid square, therefore, the management of Yarmouk Nature

Reserve should consider conserving these CWR taxa and including them in their protection strategy. Figure 3.9 also shows an area that have at least one CWR taxa close to the Shawmari Wildlife Reserve, therefore the boards of this reserve should be enlarged to include protecting those taxa and include them in their conservation strategy. Shubash Nature Reserve in Palestine have one CWR per grid square, therefore, it is recommended that the management of this site should consider including protecting those CWR taxa. It is found that in Hifa district in Israel that Carmel Mountain National Park has high priority areas with CWR taxa ranging from 6 taxa in the yellow to 11 taxa the dark red, therefore the management plan for this side should be adjusted to include those CWR taxa in their strategy.

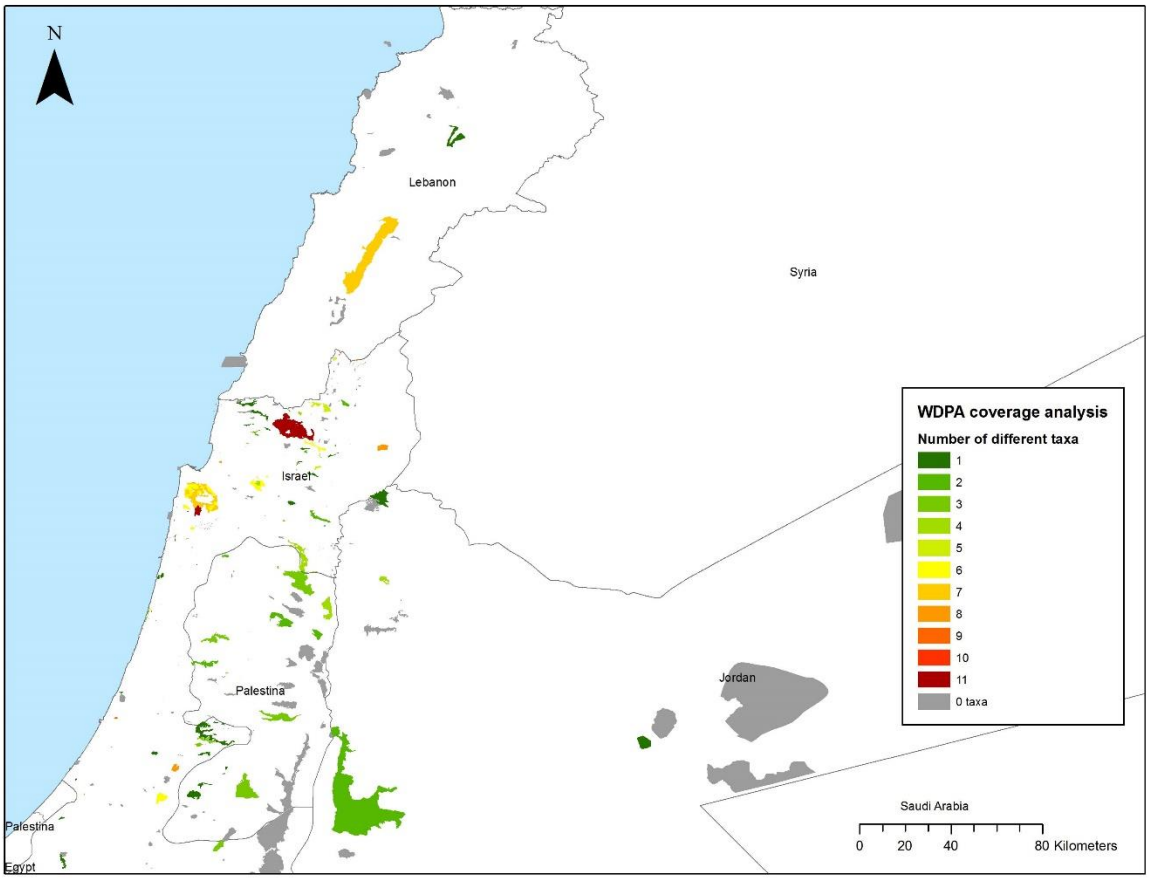

Figure 3-9 A zoom in some interesting area where there are PA with highest values using ArcGIS Pro 2.4.

Occurrence records were displayed in Figure 3.9 and the result obtained can be seen in Figure 3.10. Hence, Figure 3.10 shows a closer view in some interesting area where

there are PA with highest values of CWR taxa adding the layer of occurrence records using ArcGIS Pro 2.4. The reason for this analysis is to show where these CWR exist precisely. As an example, more occurrence records are found in the Eastern side of the Mujib Biosphere Reserve in Jordan. Therefore, the management of this Reserve should pay attention to their locations and protect them. Figure 3.10 indicates that occurrence records are concentrated around Al Shouf Cedars Nature Reserve in Lebanon so the boarder of the Reserve should be enlarged to conserve these sites.

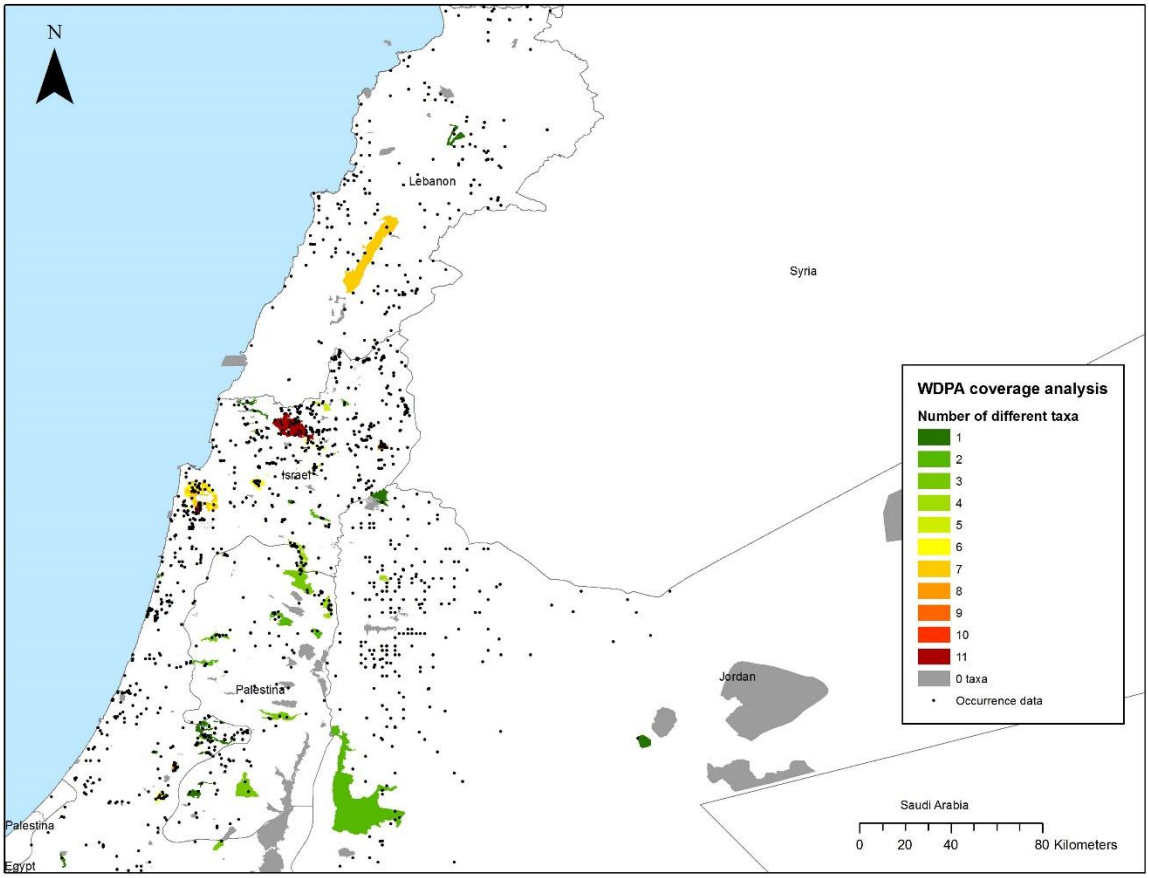

Figure 3-10 A zoom in some interesting area where there are PA with highest values with occurrences using ArcGIS Pro 2.4.

Figure 3.11 shows some unusual point distribution noted associated with georeferencing from coordinate systems UTM (grids) which represents low quality (despite GEOQUAL values are not so low. It was noted in Jordan where they use this type of coordinate system, because that distribution only appears there using ArcGIS Pro 2.4.

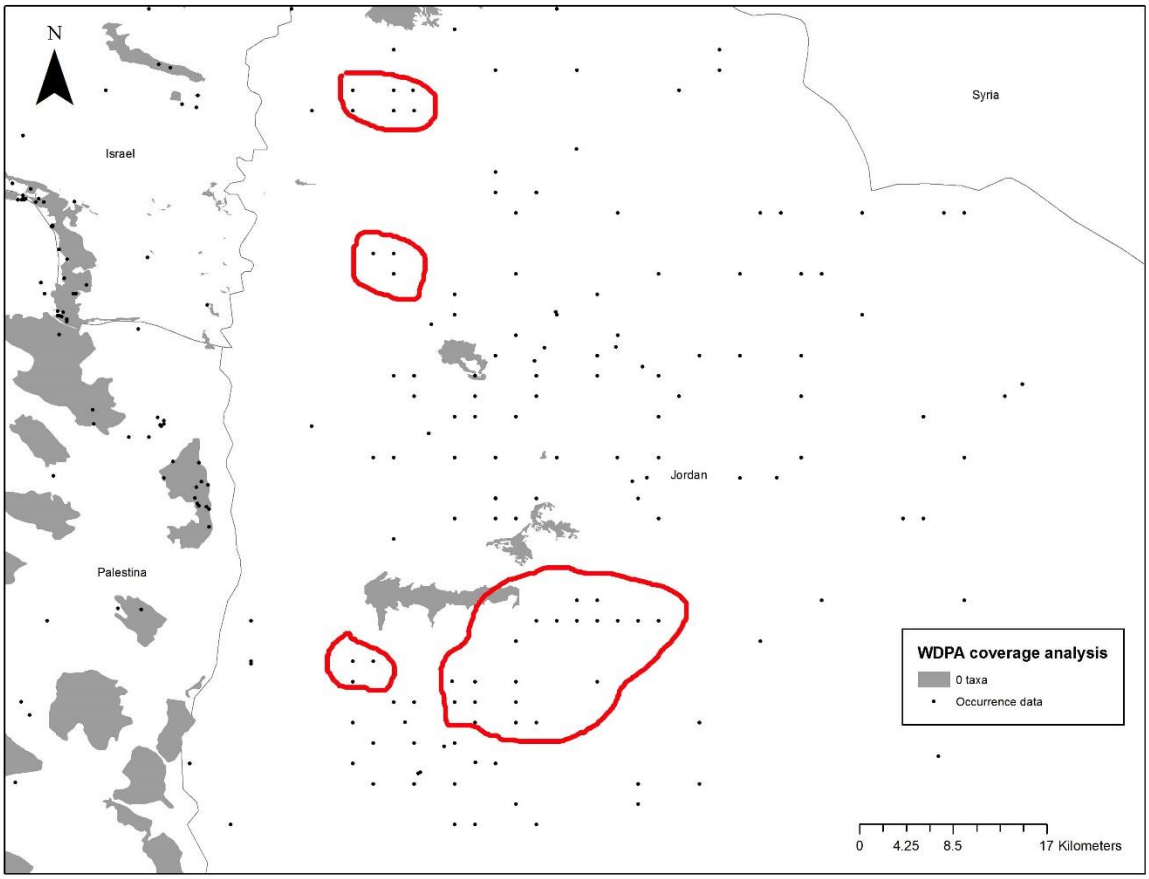

Figure 3-11 shows some unusual point distribution noted associated with georeferencing from coordinate systems UTM (grids) which represents low quality using ArcGIS Pro 2.4.

Supplementary material 1 in the annex contains the R script used to run the complementarity analysis. It corresponds 100% to the Complementa tool script, but with some initial parameters manually introduced in order to run the script in R (without the use of the friendly version of the tool). It also contains the WDPA and "pasaporte" files, required to run the script. Figure 3.12 displays the cell complementary analysis for the complete list of target countries with a grid cell of 5 arcs minutes-10 km2 using Arc GIS Pro 2.4.

The Complementa Target Countries analysis contains results from Complementa tool for both complementary cells (5 arc minutes-10 km2 at Equator cell size) and protected areas' analysis, however this last uses PA maps with less or null representation for some countries (i.e. Turkey and Syria). Most complete cell analysis can be found in this analysis for all the data used. Several priority grid squares were established. Each

grid square colour represents the number of CWR taxa it contains. The blue square contains 36 CWR taxa, the light blue contains 20-35 CWR taxa, the yellow contains 9-20 CWR taxa, the orange contains 5-9, and the red contains 1-5 CWR taxa. It can be noted that the top sites with the highest CWR taxa concentration are found in eastern Turkey, with two blue grid squares containing at least 36 CWR taxa each. The next highest CWR taxa is found in north-east turkey, not far from the first two. The fourth highest CWR taxa is found in Latakia in Syria with the light blue square containing 20-35 CWR taxa. The fives, sixth, seventh highest CWR taxa are found in Turkey with the yellow square containing 9-20 CWR taxa, one in Izmir Province, one in Kumluca Antalya, and one in the South-eastern Anatolia Region near Diyarbakır. There are several priority squares with the orange colour containing 5-9 CWR taxa. The first one is in the Zabadani District in Syria and the rest are in Turkey. It was noticed that Jordan does not have any grid squares and in Iraq, there is only one red grid square containing 1-5 CWR taxa. In Syria there are three red grid squares

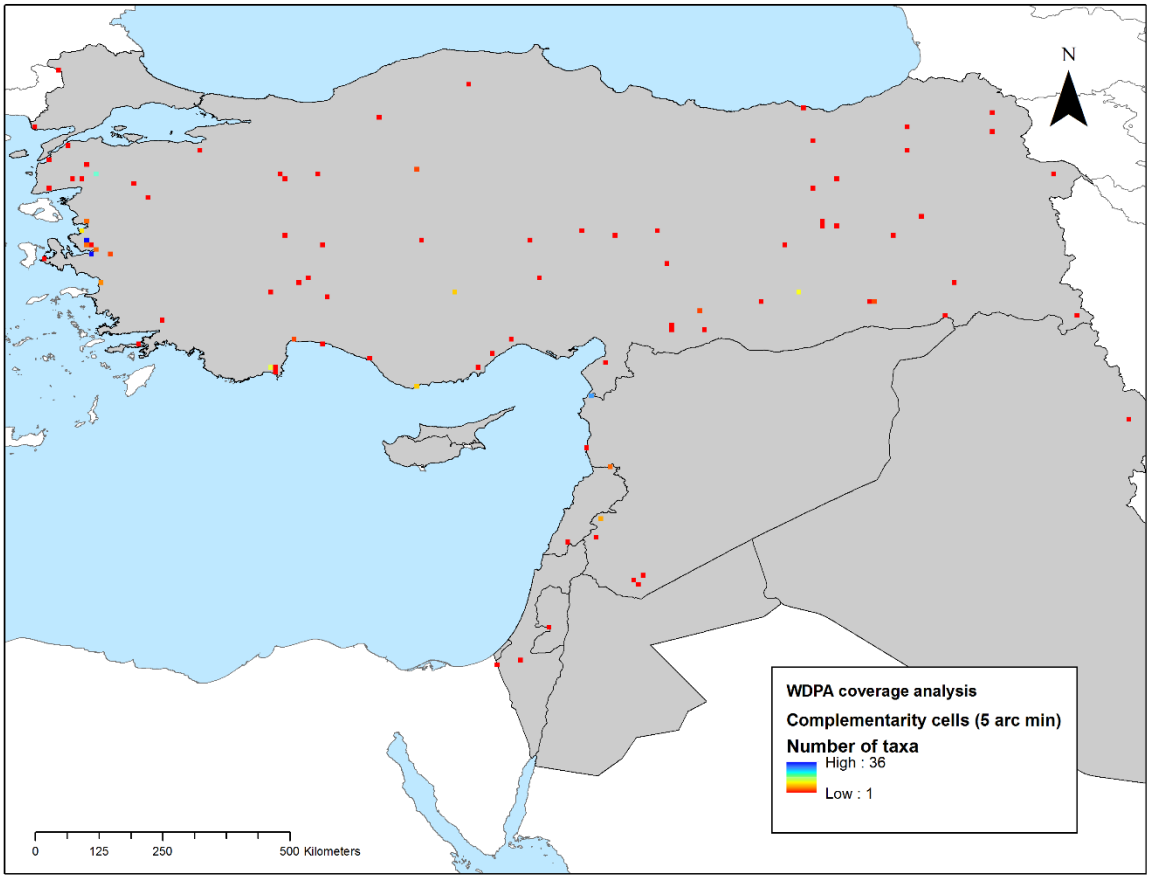

Figure 3-12 the cell complementarity analysis for the complete list of target countries with a grid cell of 5 arc minutes-10 km2 using ArcGIS Pro 2.4

containing 1-5 CWR taxa close to each other at As Suwayda and this site need conservation.

Zooming on the most interesting areas would be beneficial for this analysis to get more focused map with a grid cell of 5 arcs minutes-10 km^2. The result can be seen in Figure 3.13. This area in Eastern Turkey especially in Izmir Province have the highest concentration of propriety grid squares and contains two blue grid squares containing at least 36 CWR taxa each. This area confirms to previous published literature that Turkey is one of the countries with the highest CWR per unit area.

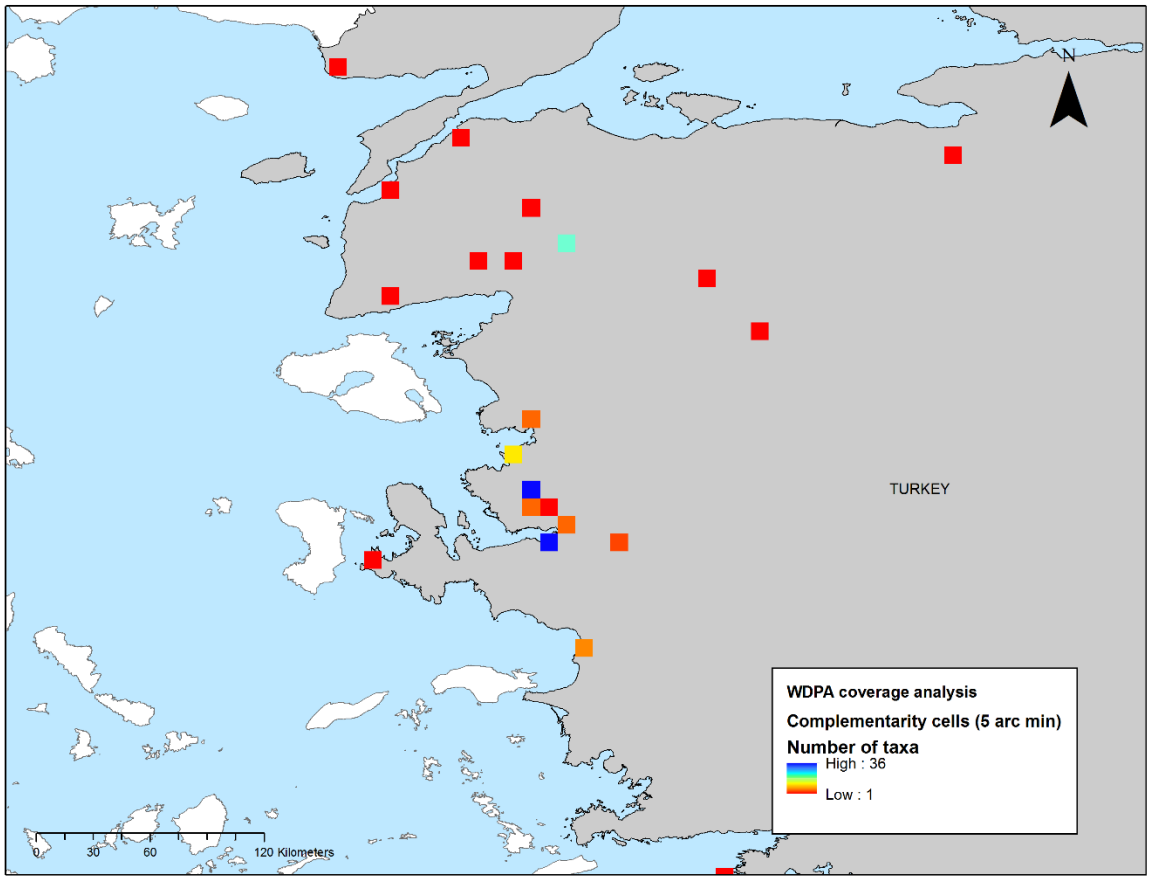

Figure 3-13 zoom on the most interesting areas with a grid cell of 5 arc minutes-10 km2 using ArcGIS Pro 2.4.

Figure 3.14 shows a closer look at only one point in one of the blue cells. It attracts attention, having the highest concentration of propriety grid squares and containing at least 36 CWR taxa.

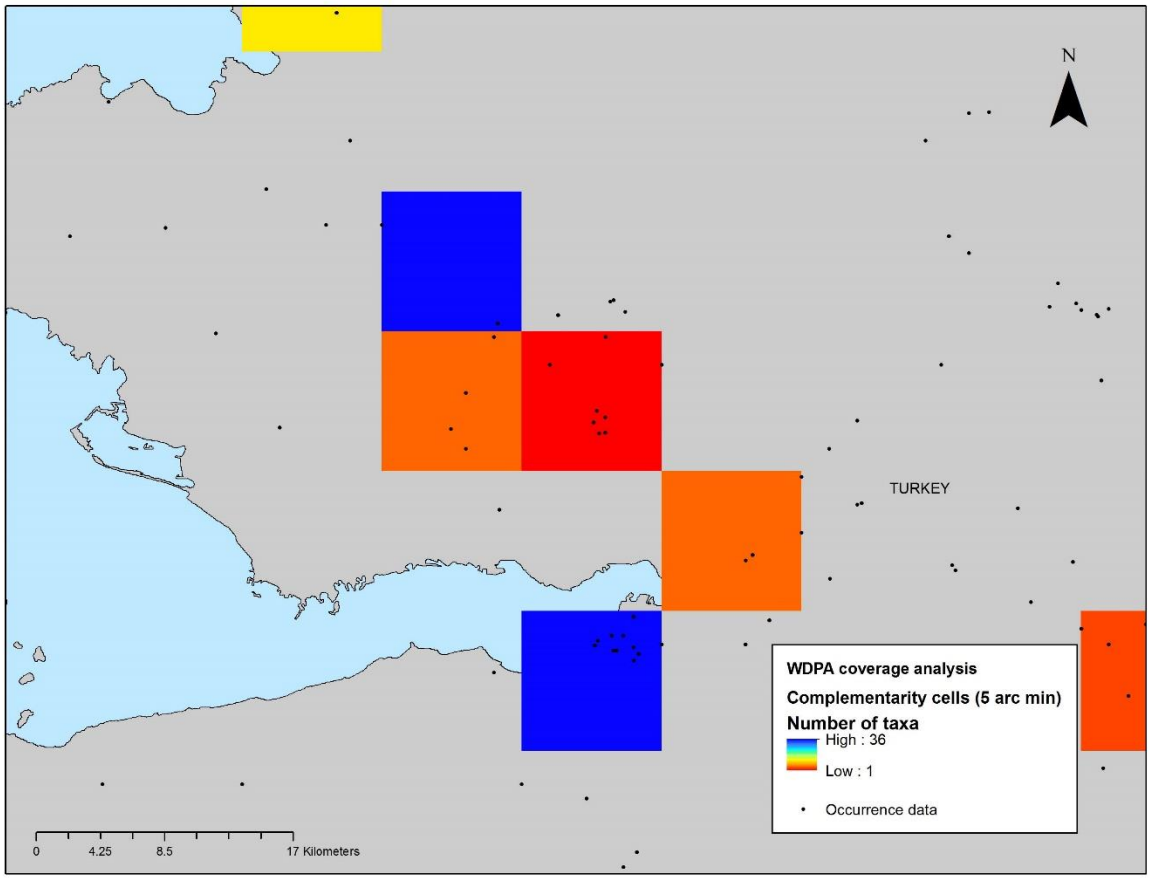

Figure 3-14 shows only one point in one of the blue cells with a grid cell of 5 arc minutes-10 km2 using ArcGIS Pro 2.4.

3.7. DISCUSSION

One of the purposes of this study was to create a regional database of occurrence records for the Fertile Crescent priority CWR. To achieve this, 23,878 records were collated. The methods used to find the richest hotspots for CWR diversity in the Fertile Crescent are in line with previously published methods, such as the ones proposed by Fielder *et al.* (2015) and Phillips *et al.* (2016).

The knowledge generated will enable policymakers to implement effective protocols to conserve CWR. CWR play an essential role in current and future food security strategies. They have been used as a source of diversification for domesticated crops and have contributed to improved yield by introducing genes that confer resistance to insects and plant diseases, tolerance to salinity stress, drought, and extreme weather conditions. There is a broad diversity of CWR throughout the Fertile Crescent, and this study is aimed at recommending candidate genetic reserves

intended for active CWR conservation as a keystone for implementing a regional conservation strategy for such important genetic resources.

The main recommendation of this paper is the implementation of proposed CWR genetic reserves whether the outcome from Maxent and Diva GIS or the outcome from the complementarity analysis using CAPFITOGEN. Both results are important and can be both used in combination with each other to find the best outcome, although each software developer of those applications claims their methods are the best. The outcome of this study is significant, as the results from the analysis of occurrence data are critical to conserve CWR. Although several publications mention some of the biodiversity hotspots in the region, most of them are focused on a particular genus. Shehadeh (2011), as an example, identifies a hotspot in Syria, in the Tel Kalakh area, for *Lathyrus* taxa diversity and another hotspot in Turkey, in the Osmaniye province, for *Lathyrostylis*.

Based on Maxent and Diva GIS analysis, the richest hotspots for CWR diversity have been found in Northwest Syria, Northern Lebanon, and Western and Eastern Turkey, including the Ankara region. Spots for CWR protected areas for the Fertile Crescent have also been recommended. Site 1, Tel Kalakh, is relatively close to the Quttina Lake protected area near Homs in Syria, and site 2, Izmir, is relatively close to the Gediz Delta protected area, a Ramsar Site in Turkey. However, both sites appear to be unsuitable habitats for CWR *in-situ* conservation. Therefore, active *in-situ* CWR conservation in the Fertile Crescent will require that either new protected areas are established, or active *in-situ* conservation is promoted in less formally managed sites. The complementarity analysis using CAPFITOGEN VERSION 2.0 found that the top sites with the highest CWR taxa concentration are found in eastern Turkey which is in line with site two in Izmir established by Maxent and Diva GIS analysis. Both analyses can be used in conjunction with each other.

These locations for CWR protected areas are vital towards the conservation of our genetic resources to help our planet fight against climate change and other threats to agricultural biodiversity and food security. This study provides the minimum biodiversity hotspots needed.

In the future, there is a need to combine the taxa richness with potential richness for adaptive traits which can increase the number of recommended protected

areas. A trait can be defined as adaptive if it is suitable to survive in new natural environmental conditions (Ackerly *et al.*, 2000). To elaborate, only CWR taxa that have adaptive traits for climate change and other environmental stress, resistance to pests and diseases, and ability to increase yield in the Fertile Crescent will be selected to find genetic reserves for them.

The results indicate that the gaps in the representation in gene banks need to be filled, especially for high-priority under-represented taxa related to barley, sorghum, oat, pea, sugar, beet, rye and sugarcane. Further studies are required, such as climate change assessment, to study the impact of climate change on these CWR taxa.

After carefully examining the representation of priority CWR in global gene banks, it can be concluded that there is a lack of representation in gene banks and an urgent effort to conserve them *ex situ* is required.

To fill the gaps in conservation, seeds need to be collected from areas rich in CWR that have been outlined in the *ex situ* gap analysis map through site visits. The collection mission could be done by national and regional gene banks with the aid of universities, local communities, and governmental departments. Duplicates of the seed samples then have to be sent to international gene banks such as the Svalbard Seed Vault.

Collected CWR seeds should also be crossed with domesticated crops to transfer the desired genes based on the gene pool assessment. More advanced techniques such as *in vitro* gene transfer could be done for CWR taxa that are difficult to cross using the natural breeding methods.

The gap analysis method using MaxEnt Version 3.4.1 and DIVA-GIS is an effective calculation method to detect geographical areas rich in CWR and also taxa that are under-represented. Using the number of germplasm accessions in the assessment is an effective method in the gap analysis because if the number is low, the priority for collection is increased. The FPS is used to effectively identify priorities that not only rely on the number of germplasm accessions but also on the number of samples and other factors.

3.8. CONCLUSION

A regional database of occurrence records has been created for CWR in the Fertile Crescent.

The richest hotspots for CWR diversity have been identified in the Fertile Crescent and are located in Syria near the Lebanese border and the Syrian Coastal Mountain Range in north-western Syria, north-western Jordan and several places in Turkey. Ten virtual CWR genetic reserves have been recommended for the Fertile Crescent using Maxent and Diva GIS. A complementarity analysis using CAPFITOGEN has also been performed and it was discovered that the top sites with the highest CWR taxa concentration are found in eastern Turkey. Both the data and methodology applied can be used in setting strategies to conserve CWR plant genetic resources. This idea was raised to help the Fertile Crescent meet its targets in conserving CWR diversity and ensuring that CWR genetic resources are preserved to prevent and tackle global food insecurity.

The *ex-situ* gap examination shows that 30% of CWR taxa have no representation in gene banks, and only 70% of the examined CWR taxa are represented. Significant gaps in *ex-situ* conservation occur in the west and south of Turkey across the Mediterranean seashore, North Lebanon, and west of Syria (in Lattakia and Tartus Governorate), across the border between Turkey and Syria, and Northern Iraq.

4. CHAPTER 4: PROJECTED CHANGE IN DISTRIBUTION PATTERNS OF CROP WILD RELATIVES UNDER CLIMATE CHANGE: A CASE STUDY OF THE FERTILE CRESCENT

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4.1. ACKNOWLEDGMENT OF COLLABORATIVE WORK

Author contributions: Wathek Zair collected the data. Wathek Zair analysed the data. Wathek Zair wrote the chapter. Nigel Maxted, Joana Magos Brehm, Ahmed Amri reviewed the manuscript. Wathek Zair edited the chapter.

4.2. ABSTRACT

The aim of this paper is to evaluate the changes in geographical distributions of priority crop wild relatives (CWR) in the Fertile Crescent region.

4.3. METHODS

A set of 441 priority CWRs were included in this analysis. A database of 23,878 occurrence records was created by collecting species distribution information. Current and future climate data were gathered from WorldClim. MaxEnt Version 3.4.1 was used for species distribution modelling (SDM) using current and projected climate data. Two dispersal scenarios were considered. The first assumes that the wild relative taxa in the analysis are incapable of tracking their preferable weather conditions, while the other assumes that CWR are capable of tracking suitable climates to ensure their survival. The maps were processed in DIVA-GIS Version 7.5.

4.4. RESULTS

Aegilops bicornis, a wild relative of Bread Wheat, and *Triticum monococcum*, a wild relative of wheat, are expected to be highly impacted by climate change. Moreover, the dispersal of *T. monococcum* is predicted to move toward the north as new suitable areas are likely to be available in northern Iraq. *Cicer bijugum*, a wild relative of chickpea, *Vicia grandiflora*, a wild relative of common vetch, and *Beta corolliflora*, a

wild relative of sugar beet, are expected to be slightly impacted by climate change, as their potential distribution areas were estimated to be reduced.

4.5. MAIN CONCLUSIONS

The impact of climate change on the distributions of crop wild relatives of crops in the Fertile Crescent is presented.

4.6. KEYWORDS

Environmental Niche Modelling, Crop Wild Relatives, Climate Change, Food Security, Genetic Diversity, Plant Genetic Resources.

4.7. INTRODUCTION

Plants are vulnerable to climate change as they cannot change their locations quickly to keep up with the speed of climate change (IPCC, 2014). Climate change impacts on the water cycle which can influence the distribution of vegetation, the rise in CO_2 concentration in the atmosphere has a direct impact on the respiration and photosynthesis enzymes in the plants. Increased CO_2 concentration will result in an increase in photosynthesis as well as respiration (Gonzalez-Meler and Taneva, 2004). It was thought that by increasing the rate of carbon dioxide concentration, photosynthesis will increase, which led to growth increase. However, a high concentration of carbon dioxide decreases the pace of respiration (Kidd reported it early in 1916) and many studies point out a significant potential for the impact of increasing CO_2 concentration in decreasing plant respiration (Amthor, 1997; Drake,1997Moreover, it was acknowledged that doubling the CO_2 level can cause stomata in plants to close partially, consequently decreasing CO_2 intake (Erice *et al*, 2006). Xu (2015) illustrates that a high level of atmospheric carbon dioxide concentration can cause a reduction in the total weight of winter wheat (*Triticum aestivum*), due to decreasing stomatal length and stomatal density.

Climate change will impact on plant flowering timings. When temperature is increased, plants tend to flower earlier (Fitter and Fitter, 2002). Gezon *et al.* (2016) did an experiment in the US on the wildflower *Claytonia lanceolata*. Gezon *et al.* (2016) found out that when snow was removed from around the plant, the plant flowered 10 days earlier and the flowers were partly damaged by frost as a result of earlier flowering.

Climate change will also affect pollinators (Deutsch, 2008). In the tropical area, where there is a higher concentration of insects, insect population will be affected negatively by raising the temperature as tropical area insects already live in their optimum climate condition and altering temperature will reduce their population and impact negatively on pollination.

In the cold areas of the world, where insect population is already low, increasing temperature will lead to an increase in insect population and pollination percentage will increase (Deutsch, 2008). However, Biesmeijer (2006) stated that if plants went extinct then pollinator populations which depend on those plants will be reduced (Biesmeijer, 2006).

Wheat cultivation will be impacted directly by climate change as yield will decline in latitudes from 0 to 30. The loss of yield will be due to high temperature as well as drought. For this reason, new wheat varieties are needed that can withstand abiotic stress associated with climate change (Ortiz *et al.*, 2008).

The attention is on CWR to use them in breeding programmes to increase crops' survival under the new climate change conditions. The genetic diversity of CWR is large so they can be utilised to identify genes that can tolerate biotic and abiotic stress (Dempewolf, 2017). These species are threatened and more attention should be put on them to conserve them *in situ* and *ex situ* (Dempewolf, 2017).

Jarvis *et al.* (2008) studied the impact of climate change on crop wild relatives of potato, cowpea, and peanut. Their study suggests that 16 to 22% of CWR will become extinct and half the taxa will lose their population extent (Jarvis *et al.*, 2008). It was suggested that for any conservation work for CWR, it is necessary to study the impact of climate change on those CWR taxa to see the one that will be lost so their seeds can be collected for *ex-situ* conservation in gene banks (Jarvis *et al.*, 2008).

Zhang (2017) studied the impact of climate change on crops and estimated that there will be a reduction in yield by the end of this century. The decline in yield will amount to around 36% decline in rice, 18% decline in wheat and 45% decline in corn in China (Zhang, 2017). As the reduction in yield is expected, it is advisable to use crop wild relatives in breeding programmes to increase crop performance, especially in the Fertile Crescent context when drought was recorded as a result of climate change (Kelley *et al.*, 2015).

Pour-Aboughadareh (2017) studied CWR in wheat and found that CWRs are an important plant genetic source that can be used to transfer genes that are tolerant of adverse abiotic and biotic conditions. Four species of CWR of wheat showed tolerance to drought (Pour-Aboughadareh, 2017). This CWR should be used in breeding programmes (Pour-Aboughadareh, 2017) as a way to mitigate the potential impact of climate change.

Phillips *et al.* (2017) studied the impact of climate change on CWR in Norway. The study found that under climate change, CWR will move their locations to the northern areas of Norway and the number of threatened CWR species will increase (Phillips *et al.*, 2017).

An investigation of the impact of climate change on the distribution of CWR in the Fertile Crescent is displayed in this study. GIS tools were applied to investigate the impacts of climate change on the future distribution rang of 441 CWR taxa in the Fertile Crescent. The result helps to enhance the conservation of CWR *in situ* and *ex situ* and to achieve the conservation strategy for the Fertile Crescent as a global centre for agrobiodiversity and to ensure food security.

4.8. METHODS

4.8.1. Occurrence data collection

CWR priority list for the Fertile Crescent were selected for the analysis (Zair *et al.*, 2019). The list contains 441 CWR taxa (Supplementary Table 1). A database of 23,878 occurrence records was created by collecting species distributions data from databanks, gene banks, and herbaria (Supplementary Table 2). The passport data consisted of the name of the taxa, the geographical boundaries of the sample (country name), the longitude and latitude, the name(s) of the person(s) who collected it, and the institution name. Some occurrences were initially supplied without any latitudes and longitudes data.

GEOLocate (REF) was used and only the description with an exact range of <5km were taken. The dataset was standardised and a two-stage verification procedure was undertaken – one to validate the botanical nomenclature of each individual record of a species using GRIN (Boyle *et al.*, 2013), and TaxonStand (Cayuela *et al.*, 2012), and the other to validate the coordinates (longitude and latitude).

The verification of geographical coordinates involved mapping the occurrence records over the Fertile Crescent raster to detect and delete offshore coordinates (Warren *et al.*, 2013) and locations outside the named geographic zone (Hijmans *et al.*, 1999).

4.8.2. Bioclimatic data collection

WorldClim was used to obtain 19 sets of layers or environmental variables (such as elevation, precipitation, etc.) with a spatial resolution of 2.5 arc minutes (4:6 km at the equator) (Supplementary Table 16). Supplementary Table 16 in the supplementary material summarises the set of layers of environmental variables (such as elevation, precipitation, etc.) that was obtained from WorldClim (an online database) with a spatial resolution of 2.5 arc minutes.

4.8.3. Species distribution modelling

MaxEnt Version 3.4.1 software was applied in this analysis. MaxEnt Version 3.4.1 takes as input a group of layers or climatic and environmental factors (such as elevation, precipitation, etc.), in addition to a set of georeferenced occurrence coordinates, and creates a model of the series of the specified species.

MaxEnt Version 3.4.1 was chosen for many reasons. First, MaxEnt Version 3.4.1 allows users to distinguish the species distribution using georeferenced occurrence locations only. Secondly, MaxEnt Version 3.4.1 is used particularly in conservation and ecological studies (Elith *et al.*, 2006; Phillips *et al.*, 2006).

The data needed by MaxEnt Version 3.4.1 to establish SDM are as follows: georeferenced occurrence locations with a clear geographical position (longitudes and latitudes of the taxa), and a set of layers or environmental variables that the programme will use, such as elevation, precipitation, and others.

It should be noted that SDM was only formed for species with more than 10 unique georeferenced occurrence records. This is because models formed with fewer records are unlikely to produce good results or highly variable predictions, consequently predicting badly the environmental habitat of the species examined (Pearson *et al.*, 2007; Wisz *et al.*, 2008).

WorldClim (www.worldclim.org) was used to obtain a set of layers or environmental variables in Supplementary Table 16 which was uploaded to MaxEnt Version 3.4.1 (Hijmans *et al.*, 2005). The initial set of layers of climate variables were

chosen as provisional explanatory variables for all models given that they exist together with their corresponding potential global warming predictions in a spatial clear layout (i.e., raster data file).

Bearing in mind that collinearity relationship among explanatory variables may influence the process of species habitat models (Dormann *et al.*, 2013), an analysis was performed to identify and correct collinearity. For this purpose, the variance inflation factor (VIF) was used because it is a multi-variable method of recognising very correlated variables and consequently adjusting the collinearity among the initial set of 19 climate layers. The variables that have a correlation threshold of >10 were not included in the analysis to be performed as model predictors.

To perform SDM, default settings were applied in MaxEnt Version 3.4.1. After training and examining each model, the set of layers or environmental variables representing the present climate were applied. The climate data were used for the years between 1950 and 2000. Binary maps were created by using the “maximum training sensitivity plus specificity” threshold because it lessens overprediction and omission faults (Liu *et al.*, 2005).

To measure the performance of the models, the area under the receiver operating characteristic (ROC) curve (AUC) was applied. An AUC rate of >0.7 was seen as significant for this analysis because models with an AUC rate of >0.7 are seen to be capable of determining the locations where a taxon could occur.

The Representative Concentration Pathway (RCP) 4.5 for 2040–2069 (2050s) was chosen to create the SDM of the CWR because RCP exemplifies the trajectory of a stabilisation scenario in which the radiative forcing is stabilised close to the end of 2100 (Thomson *et al.*, 2011), supposing that international efforts to control the emissions of CO_2 are applied through programmes of planting more trees, maximising crop production, and altering diets (van Vuuren *et al.*, 2011).

An ensemble set of the RCP 4.5 climate predictions for the future of the set of bioclim variables, which were used as environmental drivers to model the species habitat of CWR, was obtained from ccafs-climate.org.

This ensemble was created by balancing the data of 30 different global circulation models (GCMs) created by the Coupled Model Intercomparison Project

Phase 5 (CMIP5) and applied by the Intergovernmental Panel on Climate Change (IPCC) Fifth Assessment IPCC (2014).

All the climatological layers were downloaded with 2.5 arc minutes' res, applying the empiric delta method of Ramirez-Villegas and Jarvis (2010).

Potential SDM were shaped by predicting models trained with the current climate data onto future climate predictions. Binary maps were created by applying the "maximum training sensitivity plus specificity" threshold. The next step was to reclassify the maps produced into values of 0 and 2. "0" signposts the locations that do not meet the requirement of the environmental conditions of the species, while "2" indicates the locations with appropriate environmental conditions, and therefore highly expected to contain the species analysed.

4.9. ANALYSIS OF THE IMPACTS

The current distribution of CWR has been analysis and compared to their change in suitable distributions areas as a result of climate change. DIVA-GIS VERSION 7.5 was used to map taxa richness under current and future climatic conditions.

The result of MaxEnt Version 3.4.1 was then presented in DIVA-GIS Version 7.5. Each file represents one species and can be presented in DIVA-GIS Version 7.5.

ArcGIS 10.6 tools were applied in the analysis process. The map of the future distribution of CWR taxa was then compared to the map with the current distribution to see areas of gain and loss. Two dispersal scenarios have been considered in this analysis. One is that the species can colonise the new areas. The second is the species are not able to inhabit the new areas (Peterson *et al.*, 2002; Higgins *et al.*, 2003; Thomas *et al.*, 2004). If the species are not able to inhabit the new areas, the areas of loss and gain are calculated (Riordan *et al.*, 2015). Nineteen sets of layers or environmental variables (such as elevation, precipitation, etc.) were used in this analysis (Supplementary Table 16).

4.10. RESULTS

Figure 4.1 shows the rainfall in the Fertile Crescent under the current climate conditions scenario, the projected rainfall in the Fertile Crescent under the climate change scenario, the annual mean temperature in the Fertile Crescent under the current climate conditions and the projected annual mean temperature in the Fertile Crescent under the climate change scenario.

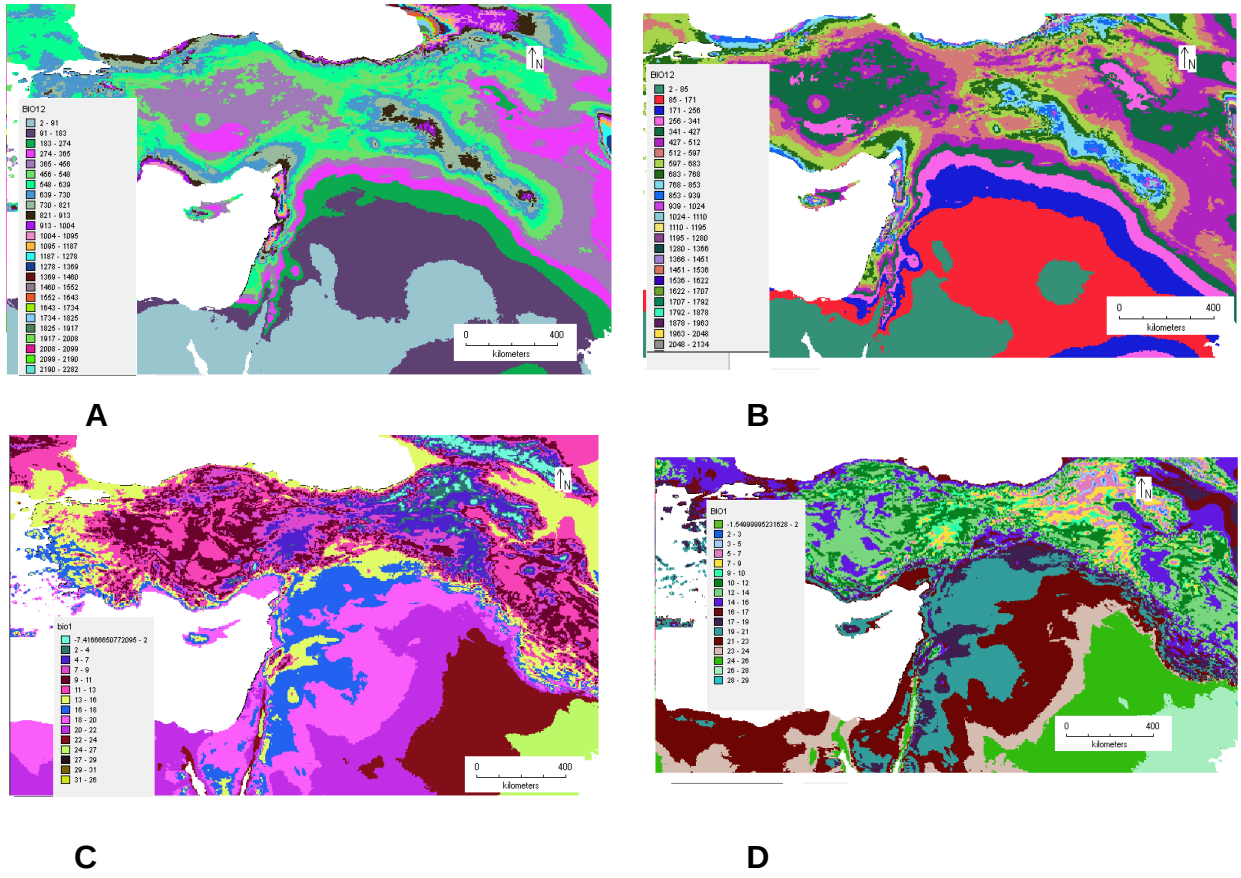


Figure 4-1. A. Rainfall in the Fertile Crescent under current climate conditions. B. Projected rainfall in the Fertile Crescent under the climate change scenario in 2100 AD. C. Annual mean temperature in the Fertile Crescent under current climate conditions. D. Projected annual mean temperature in the Fertile Crescent under the climate change scenario in 2100 AD.

As can be seen from figure 4.1 the rainfall in the Fertile Crescent desert area (Syrian Badia) in the south east part (navy blue colour in figure A and red colour in figure B) areas with similar rainfall range will change its locations slightly. The range will decrease from 2-91 mm per year in present-day to 2-85 mm per year in 2100 AD. There will be a decline of 6 mm per year in that area in the maximum rainfall range. This decline will impact on the vegetation as plants will get less water. The Syrian Badia region has low concentration of CWR, therefore, climate change impact will be minimal. However, other vegetations will be impacted. In present day the Syrian Badia is mainly utilised for grazing animals as it has sandy soil with low quality and little rainfall. Some plants in the Syrian Badia that currently exist there are *Salsola*

vermiculata, Stipa barbata, Artemisia herba-alba and *Atriplex leucoclada* (Suttie *et al,* 2005) might be impacted due to receiving lower rainfall.

The rainfall in the semi desert area in the middle part areas with similar rainfall range will change its locations also slightly. The purple colour area in figure A and pink colour in figure B) will decrease from 274-365 mm per year in present-day to 256-341 mm per year in 2100 AD. There will be a decline of 24 mm per year in that area in the maximum rainfall range. This decline will impact on barley rainfed farming as the crop will get less water and the distribution of CWR there.

Annual mean temperature in the Fertile Crescent areas with similar temperature range will change as a result of climate change between the present day and 2100 AD. The annual mean temperature in the coastal area (purple colour in figure A and blue colour in figure B) will decrease from 18-20 °C per year in present-day to 19-21 °*C* per year in 2100 AD. There will be a decline of 1 °C per year in that area in the maximum annual mean temperature range. This decline will impact on the distribution of CWR there. The potential taxon richness of 441 CWR in the Fertile Crescent under current climate conditions is shown in Figure 4.2. It can be noted that CWR are concentrated around the west side of Turkey near the city of Izmir. In such areas, CWR can reach to from 129 to 145 CWR taxa per unit area. CWR are also concentrated on the costal side of Syria, Turkey and Israel. In north west Jordan, CWR can reach to between 100 and 114 CWR taxa per unit area.

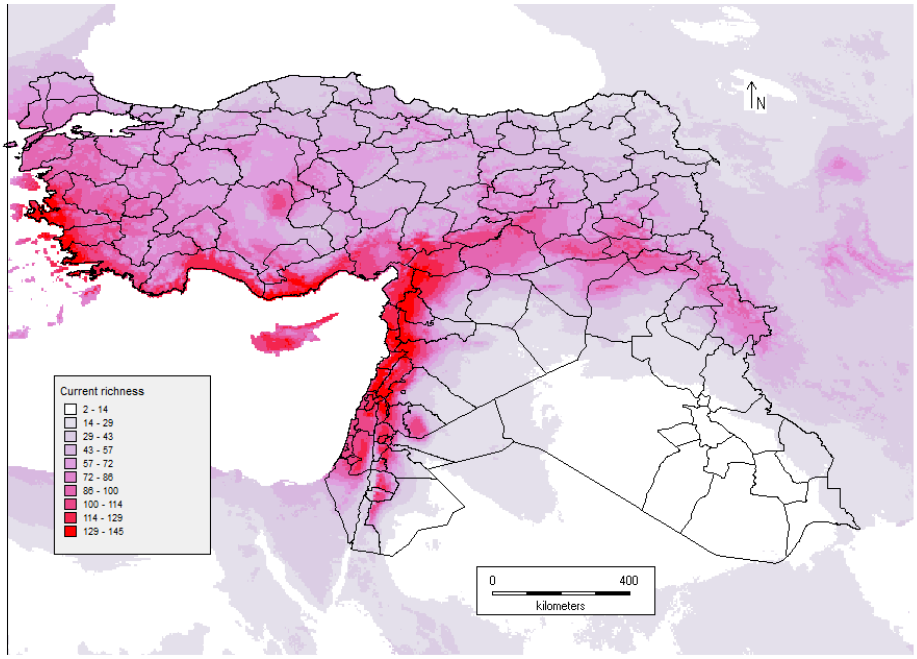


Figure 4-2. Potential taxon richness of 441 CWR in the Fertile Crescent under current climate conditions with a grid cell of 5 minutes (~9 km2).

The potential taxon richness of CWR in the Fertile Crescent under the climate change scenario is shown in Figure 4.3

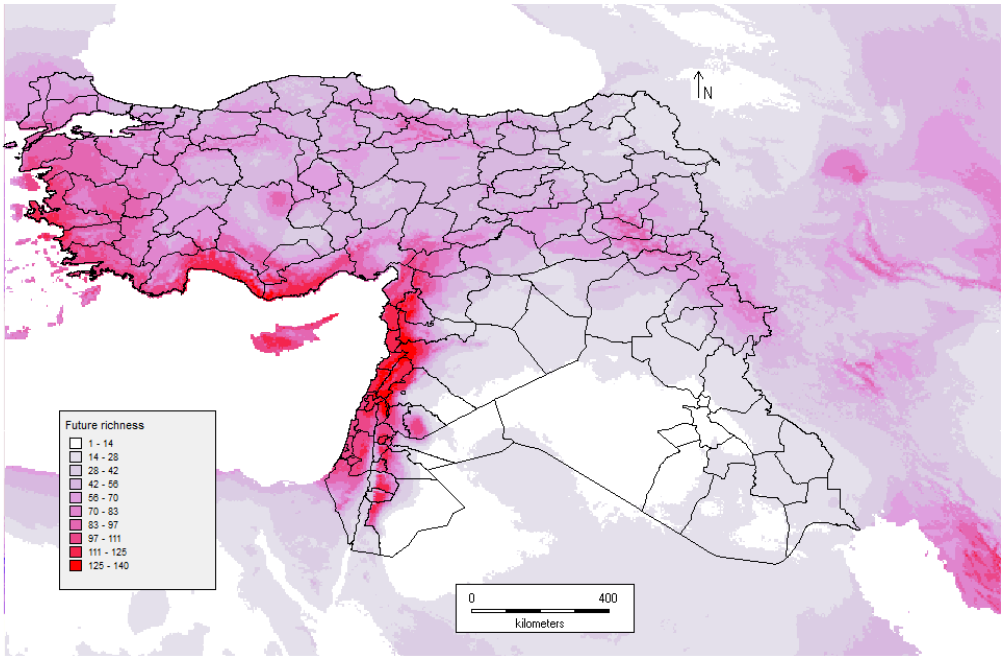


Figure 4-3. Potential taxon richness of 441 CWR in the Fertile Crescent under the climate change scenario with a grid cell of 5 minutes (~9 km2).

When comparing the two figures together Figure 4-4. And Figure 4-3, it can be noted that CWR will decline around the west side of Turkey near the city of Izmir. In such areas, CWR can reach to between 125 and 140 CWR taxa per unit area. That accounts for 4-5 decline in the number CWR taxa per unit area. For those CWR that are also concentrated on the costal side of Syria, Turkey and Israel, their number will decline to between 100 and 114 CWR taxa. In the northwest of Jordan, CWR can reach to between 100 and 114 CWR taxa per unit area. In the northern parts of Iraq, there is an area that have between 100 and 114 CWR taxa per unit area, with the climate change the concentration will decline to 42-56 CWR taxa per unit area.

4.11. DISCUSSION

When conserving crop wild relatives, the possible effect of climate change should be considered, especially if conservation is going to be *in situ* and for the long term. The outcomes of these analyses vary between different CWRs. For this reason, it should be noted that various preservation strategies should be undertaken, depending on if the decision is to protect a precise geographical location or several taxa.

The result of the analysis in Figure 4-5 is in line with Kelley *et al*., (2015). that the rainfall in the Fertile Crescent will decrease as a result of the climate change.

The results are also in line with the IPCC (2014) result that there will be a decline of 1 °C per year in that area in the maximum annual mean. There will be a rise between 0.3°C and 1.7°C by 2100 if the world produces lower greenhouse gases, and that will increase to 4.8°C if the world produces a higher amount of greenhouse gases (IPCC, 2014). The annual mean temperature in the coastal will decrease by 1 °C between present-day and 2100 AD.

CWR will decline in the Fertile Crescent in general and some areas in Turkey in particular. This result conforms to the result obtained by Castaneda-Alvarez (2016) that the potential losses in areas for 1-5 taxa are localized in temperate regions.

In the species approach, *Beta corolliflora* as an example has a major detrimental influence on their distributions in the mentioned climate change scenario and may need to be conserved in *ex-situ* gene banks because of the substantial decline in their biologically suitable sites. However, if the species can disperse and track their suitable climate in case of climate change such as *Triticum monococcum*, extra observation of

the genetic components of their natural populations will be required because it helps in spotting a reduction in the genomic diversity of these populations at an earlier stage.

To discover whether the CWR can successfully inhabit the new location predicted, new competitors must be monitored and land-use changes plus habitat fragmentation should be observed. To make it easier to access these CWR resources for research purposes and breeding programmes, complementary *ex-situ* conservation should be applied.

Furthermore, observing the CWR taxa genetic diversity and their reaction to global warming will produce vital data on the reaction and changes in the genetic components of the populations of these species. In the geographical approach, the sites that would be selected as nominee areas for creating *in-situ* conservation must display great taxa richness and show minor changes in their potential richness because they display climatic stability.

Sites with a great richness that display high potential losses of richness might be considered inadequate for *in-situ* conservation in the long run, and thus safeguarding this genetic diversity in gene banks is necessary.

Further methods should be considered for prioritising CWR taxa and crop gene pools in the species approach in conservation. These include the socioeconomic value of the associated cultivated crop and the nutrition value, the present conservation grade (IUCN Red List), and how much the CWRs are represented both *ex* and *in situ*.

Several other factors can be selected for creating the priorities, but these depend on many factors such as available funding, the objectives of the conservation, and the geographical range of the conservation work.

From a more utilitarian viewpoint, prioritising CWRs that are less tolerant to climate change should be directed by the simplicity of crossing and breeding those CWR taxa with their related crops (taxa in the primary and secondary gene pools) because the creation of a fertile hybrid is thought to be less difficult to perform. Furthermore, such prioritisation should take into consideration more distantly related taxa (tertiary gene pool) that have previously been successfully utilised in plant breeding as sources of specific traits and genetic diversity.

4.12. CONCLUSION

The impact of climate change on the distribution of CWRs related to major crops is displayed for the Fertile Crescent.

Among the taxa assessed CWR taxa that are expected to be highly impacted by climate change are *Aegilops bicornis*, a wild relative of Bread Wheat, and *Triticum monococcum*, a wild relative of wheat. Some CWR taxa new suitable areas are likely to be available as an example, *T. monococcum* is predicted to move toward the north in northern Iraq. Some major CWR taxa are expected to be slightly impacted by climate change, as their potential distribution areas were estimated to be reduced. Those include *Cicer bijugum*, a wild relative of chickpea, *Vicia grandiflora*, a wild relative of common vetch, and *Beta corolliflora*, a wild relative of sugar beet,

The study will help to improve *in-situ* and *ex-situ* conservation of CWR. Both the result and the methodology applied can be used in setting national, regional, and global conservation strategies. The recommendations will help the Fertile Crescent meet its targets in conserving CWR diversity, as well as making sure that CWR genetic resources are preserved to prevent and tackle global food insecurity.

CHAPTER 5: THREAT ASSESSMENT OF CWRs

5.1. ACKNOWLEDGMENT OF COLLABORATIVE WORK

Author contributions: Wathek Zair collected the data. Wathek Zair analysed the data. Wathek Zair wrote the chapter. Nigel Maxted, Joana Magos Brehm, Ahmed Amri and Peter Winn reviewed the manuscript. Wathek Zair edited the chapter.

5.2. ABSTRACT

In Fertile Crescent, some CWR taxa have been assessed already using the IUCN Red List assessment. The rest of taxa has not been assessed before and some has been assessed for the Europe region only. A list of the taxa that needs an assessment has been identified in collaboration with the IUCN. It was noted that CWR taxa that are related to wheat, barley, oat, and chickpea require an assessment. Some additional CWR related to Medicago that have not been assessed before were assessed. All the assessments were done globally regardless if the taxa exist in the Fertile Crescent or not. A total of 88 CWR taxa were red list assessed, 47% of them were assessed as Least Concern (41 taxa), 28 % of the total were assessed as Near Threatened (25 taxa), 21% as Data Deficient (18 taxa), 3% as Endangered (three taxa) and 1% as Critically Endangered (One taxa).

5.3. INTRODUCTION

In the Fertile Crescent as part of the WANA region, 10% of plant species were identified as threatened on some level (Jaradat, 1998). Since more crop species have been subjected to risks of loss, an effective conservation strategy is urgently needed. Many researchers have linked the causes of threat to the increase in human population, habitat loss, fragmentation, degradation, overexploitation, spread of exotic and invasive species, changes in agricultural practices and land use, natural catastrophes, climate change, and lack of conservation programmes (Gomez-Campo, 1987; Groombridge, 1992; Janetos, 1997; Jeffries, 1997; Primack, 2001, 2002; Stedman-Edwards, 2000; Oostermeijer, *et al*., 2003). Several deliberate attempts and efforts have been made to find methods for assessment of threats affecting plant biodiversity including CWRs. Threat assessment contributes to a reduction in genetic erosion, especially for those species and populations at risk (Keith and Marion, 2002). In the Fertile Crescent, there was a threat assessment study conducted in Syria on CWR from the *Vicia* genus. The study illustrates that there is a decrease in the size of

the population over 20 years (Keisa *et al.*, 2008). The methods used are designed to compare the population size before and after 20 years. Also, there is an assessment questionnaire adapted from Guarino (1995, 1999) and de Oliveira and Martins (2002) as well as Goodrich (1987) before them to assess the threat. The threat assessment could be implemented using available data of taxa and the area without the need to conduct a site visit. The model works by scoring a set of parameters, such as the abundance of the taxon, the level of agricultural development, and the proximity and intensity. Burgman *et al.* (1999) suggest several prioritisation methods for conservation based on four areas: (i) Qualitative risk assessment; (ii) Point scoring procedures; (iii) Rule sets; and (iv) Population viability analysis (PVA). According to Mace and Kershow (1997), implementing any of the proposed methods to efficiently assess the threatened species needs to be objective and comparable. The threat factors are subject to the way of their usage in monitoring threats of Plant Genetic Resources (PGR). A rare population, as an example, is not always an indicator that the population is at high risk (Mace and Kershow, 1997). Mace and Lande (1991) clarify that not all methods of threat assessment are accurate to assume a species is at risk or not. For that reason, there would be a lack of coherence and reliability (Burgman *et al*., 1999) resulting in different views. Burgman *et al*. (1999) suggest that there will be no single protocol compatible with all cases of threats assessment. Any threat assessment should be subject to objectivity and comparability. Accordingly, using a uniform classification system will be helpful to sort out species regarding the hazards of species extinction. This will help to specify a lot of endangered species (Ford-Lloyd *et al.*, 2008).

Measuring plant species population over a period is not an indicator of the decline in species genetic resources as other factors should be considered such as if the species are already conserved *ex situ*. The IUCN Red List assessment has now been used broadly to assess plant species and to see their risk status (IUCN, 2001). The IUCN include *ex-situ* assessment of plant genetic materials (IUCN, 2001). Ford-Lloyd *et al.* (2008) indicate that if a certain number of species are at a high risk of a threat then they should be a high priority for conservation (Ford-Lloyd *et al.*, 2008). There is an online assessment course that takes place before any assessment is undertaken, and it is important to take the course to make a right decision when assessing species.

After the online course was completed, the assessment started. This assessment can be applied to plants as well as animals (IUCN, 2001). Figure 5.1 explains the IUCN assessment criteria. If there is not much information about a species then it will be classed as data deficient, nevertheless normally it is advisable to get as much data as possible about the species. Online sources of information include GRIN, GBIF, and botanic garden publications are useful tools to get information about the species. For *ex-situ* assessment, information from the global seed vault and other European and international gene banks should be examined. If the species is distributed well around the world then the species might be assessed as least concern. If it was noticed that the species population has declined and there are risks that the species has been exposed to, it might be considered as vulnerable. If there is a real risk to the species and there was low population density, the species might be assessed as endangered. If the species is clearly threatened and the population is declining, then it might be assessed as critically endangered. If there is not any population of the species but there is genetic material preserved *ex situ,* then the species is extinct in the wild. If there is no presence of the species in the wild nor in gene banks or in the seed vault, then the species is extinct (IUCN, 2001). Figure 5.1 shows Red List Criteria (IUCN, 2001).

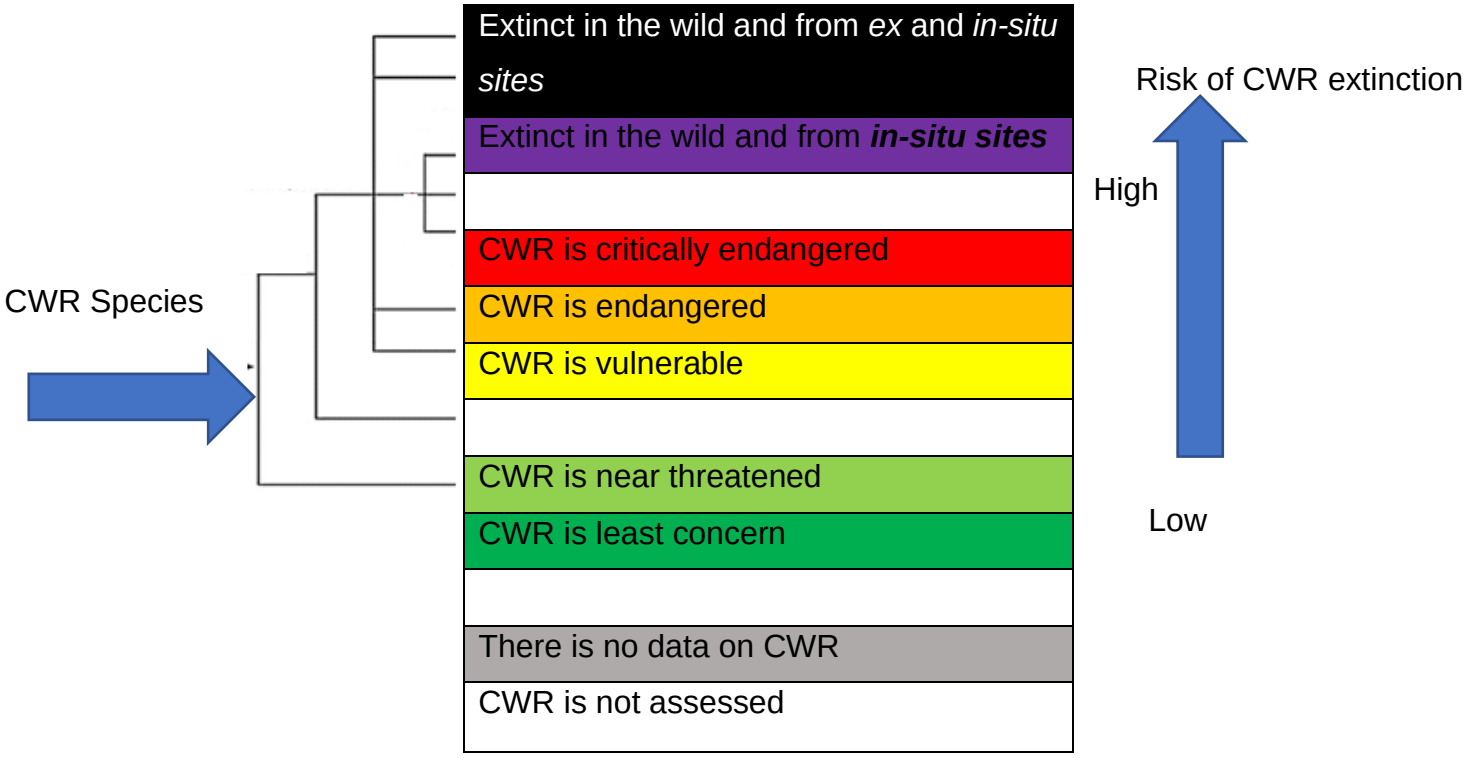


Figure 5-1. CWR Red List Criteria adapted from (IUCN, 2001)

Several other factors are included in the assessment such as fragmentation and distribution range (IUCN, 2001).

Geographical distribution could be applied in this matter to measure the endemic threatened taxa. This approach suggests that those species with limited distribution are possibly threatened, so will be given a higher priority than more widely distributed taxa. These approaches could be used on the national or global levels. Hodgkin (1995, 1997) states that it is useful for each country to establish its own CWR list as CWRs could be conserved *in situ* or *ex situ* according to their state in each individual country. In addition, the priority list of CWR could be a key part of the national inventory (Hodgkin and Meilleur, 2004). An IUCN red list assessment was undertaken for CWR which fill the gap in knowledge and assess in conserving those plant genetic resources as an aid to achieve food security.

5.4. OBJECTIVES

The objective of the study is to undertake IUCN Red List threat assessments of major CWR taxa.

5.5. METHODS

The method involved taking the IUCN Red List threat assessment course and becoming an assessor, then following the IUCN Red List Assessment guidance documents (http://www.iucnredlist.org/technical-documents/red-list-documents) and collecting the data needed for the assessment. There are fields that need to be completed and supporting data that can help with the assessment. For the required fields, scientific names will be needed for each species. the full name with the subspecies name and authority are required. As CWR are being assessed, it is important to have the full name. An example of that would be if the following taxa have been assessed *Triticum aestivum* L. subsp. *tibeticum* J. Z. Shao. If only *Triticum aestivum* was included in the assessment, it will end up with us assessing common wheat, which is why it is important to have the full name of the CWR that requires an assessment. In addition, it is necessary to have the whole name up to the kingdom. The kingdom is Plantae and the family is Poaceae in our example of *Triticum aestivum*. Authorities are also an important factor. Furthermore, it is needed to include information about where it is distributed and what countries it is native to, and it is important to see if there is any history of assessing the species regionally or internationally. After that, it is important to get the occurrence record of the species to see where it is distributed. Published papers, literature and observation can be used to see if the population is declining, increasing or if it is staying the same. It is important to get information about the habitat's preference of the species. It is required to write the references for the information. For the supporting data, it is required to have a GIS layer to show where the species is distributed. It would also be helpful to review the use and benefit of this species with references to the article (IUCN, 2012a). More criteria can be found on IUCN (2012a). Table 5.1. shows the number of crop wild relatives that were assessed in this study using the IUCN Red List Assessments (IUCN Version 3.1). A total number of 88 CWR taxa were assessed that belong to five crops which are chickpea, wheat, oat, barley and alfalfa. Those five crops are related to two families Fabaceae and Poaceae.

Table 5.1. Number of crop wild relatives that were assessed in this study using the IUCN Red List Assessments (IUCN Version 3.1) (IUCN, 2016).

Family	Genus	Related crop	The number of CWR Taxa assessed
Fabaceae	Cicer	Chickpea	5
Poaceae	Triticum	Wheat	15
Poaceae	Avena	Oat	3
Poaceae	Hordeum	Barley	2
Fabaceae	Medicago	Alfalfa	63
Total: 2	Total: 5	Total: 5	Total: 88

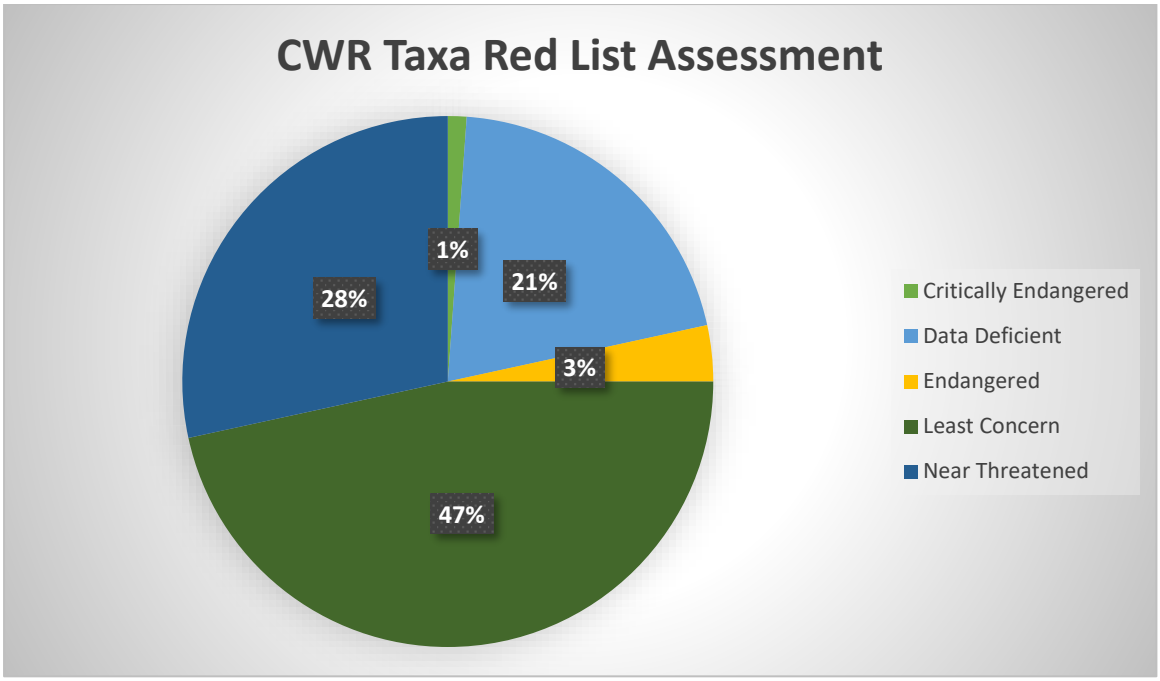
Table 5.2. Breakdown of the Number of crop wild relatives that were assessed in this study.

Genus	The number of CWR Taxa assessed	Total of taxa assessed from CWR priority list for the Fertile Crescent	Total of taxa assessed from Alfalfa and Relatives Book by Ernest Small
Cicer	5	5	0
Triticum	15	6	0
Avena	3	3	0
Hordeum	2	2	0
Medicago	63	9	63
Total: 5	Total: 88	Total: 25	Total: 63

5.6. RESULT

A total number of 88 CWR taxa were included in the assessment. The full red assessment result is found in Supplementary material 2. Those 88 CWR taxa are related to five crops that belong to two families (Table 5.1). In the Fertile Crescent, there are 441 CWR priority taxa, 25 of them have been included in the assessment. The rest of the taxa that are included in the assessment are 63 and were identified as their assessment needs an urgent update and some of them were never assessed before. The result indicates that one taxon (*Medicago halophila* - (Boiss.) E.Small) were assessed as Critically Endangered. A total of 18 taxa were assessed as Data Deficient. Three taxa were assessed as Endangered; those are *Cicer bijugum* - Rech.f., *Medicago crassipes* - (Boiss.) E.Small, and *Medicago cretacea* - M. Bieb. A total of 41 taxa were assessed as Least Concern and 25 taxa were assessed as Near Threatened.

The result of the assessment can be found in Table 5.3 below. A detailed assessment can be found in the annex.



Assessment	Number of CWR	Percentage of CWR
Critically Endangered	1	1%
Data Deficient	18	21%
Endangered	3	3%
Least Concern	41	47%
Near Threatened	25	28 %
Total	88	100 %

Figure 0.2. CWR Red List assessment result

Table 5.3. CWR Red List assessment result per genus

Genus	Critically Endangered	Data Deficient	Endangered	Least Concern	Near Threatened
Cicer	0	2	1	1	1
Triticum	0	4	0	11	0
Avena	0	1	0	2	0
Hordeum	0	0	0	2	0
Alfalfa	1	11	2	25	24

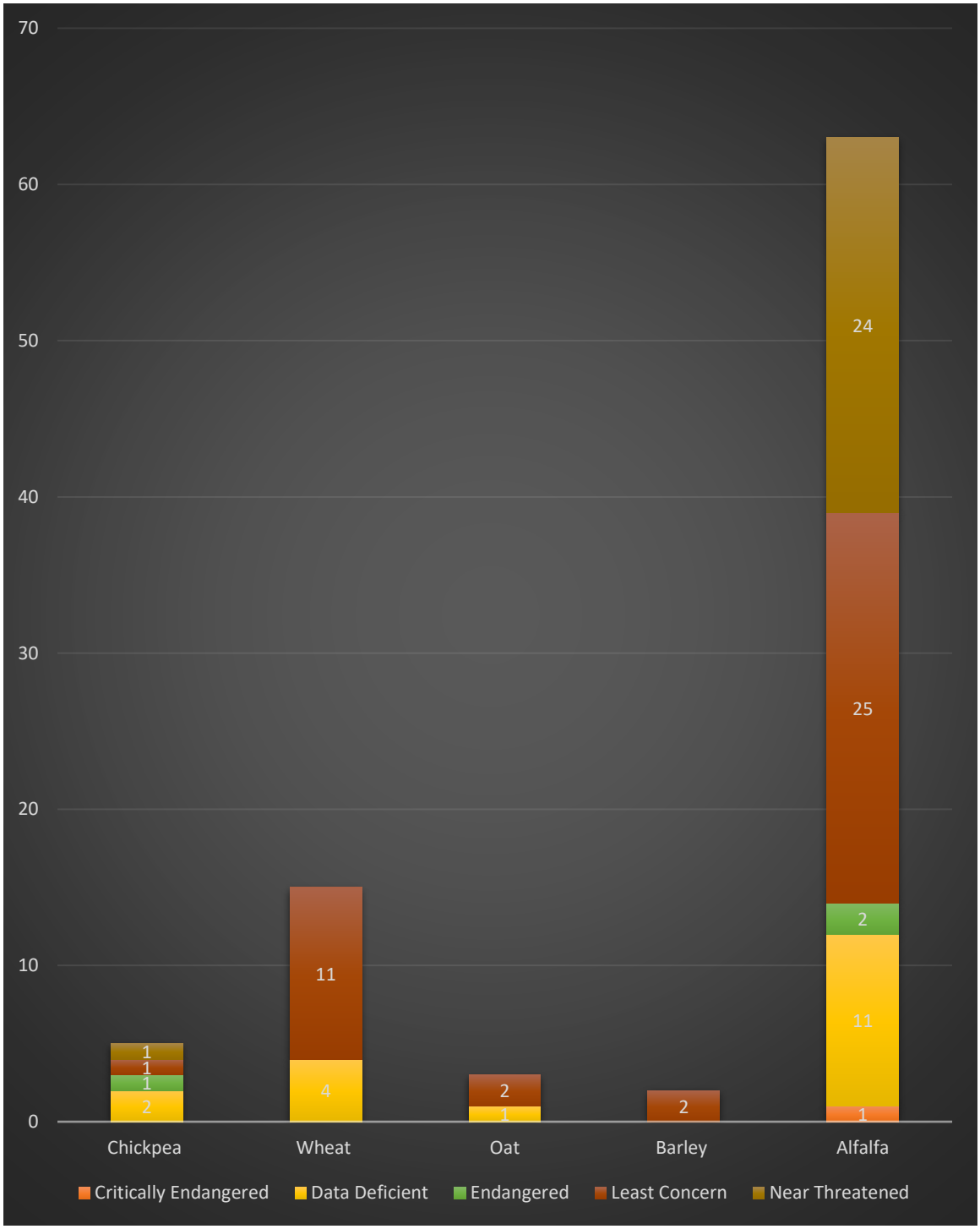


Figure 0.2. CWR Red List assessment result per related crop.

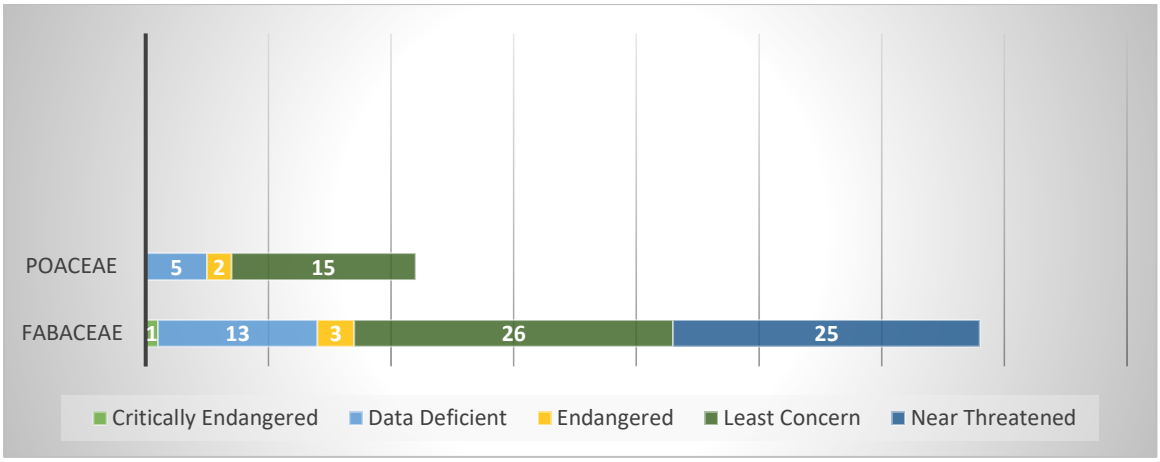


Figure 0.3. CWR Red List assessment result per family.

The reason for this section is to discuss the results further and to compare them with previously published literature about threat assessment of CWR in the region or around the world. As Jaradat (1998) illustrates that 10% of plant species were identified as threatened in the Fertile Crescent as part of the WANA region our result provides more detailed information about the threats and more precise. Our result established that 1% of the taxa assessed are Critically Endangered, 3% are Endangered, 47% are Least Concern, 21% are Data Deficient, and 28 % are Near Threatened. Having said that, it should be noted that 25 CWR out of the total 88 taxa assessed in this study are from the Fertile Crescent priority list.

It is also vital to compare our result with the European CWR assessment done by Bilz *et al.* (2011) as well as the assessment done by Taifour and El-Ohlah (2014) for CWR in Jordan. As can be seen in Table 5.4, our result is in line with the European assessment and a bit different from the Jordanian assessment. This is due to assessing different species as well as our assessment is done on a global scale for the whole planet earth rather than localised one that is focused on a area or a region. Both assessments are fine either global or regional, however global assessments are less time consuming compared to doing an assessment for each country since the financial resources are limited. The Least Concern category in our analysis contributed to the majority of the CWR assessed (47%) and that explained why the global assessment has more CWR listed in this category. For the Eu assessment, the majority of the CWR assessed as Least Concern also (*54.7%). For Jordan,* the majority of the CWR assessed are Vulnerable 87.048 %. The Endangered category has similar range in all three assessment

Table 5.4 a comparation of the red list assessment result with previously published literature.

Assessment	Percentage of CWR in our study out of 88 CWR taxa	Bilz et al. (2011) assessment for the 572 CWR for the EU	Red list Assessment for the 925 CWR taxa in Jordan (Taifour and El-Ohlah *(*2014)
Extinct			(19 taxa) 2.05 %
Critically Endangered	1%	3.3%	(1 taxa) 0.1 %
Data Deficient	21%	29%	(54 taxa) 5.832 %
Endangered	3%	4.4%	(33 taxa) 3.564 %
Vulnerable	-	3.8%	(806 taxa) 87.048 %
Least Concern	47%	54.7%	(11 taxa) 1.188 %
Near Threatened	28 %	4.5%	(19 taxa) 2.05 %

Another assessment that is done on CWR in the Fertile Crescent region partially which is the assessment based on the related crop. The highest number of Near Threatened CWR taxa are related to Alfalfa because more Alfalfa are included in this study. The highest number of Critically Endangered and Endangered CWR taxa are also related to Alfalfa. Wheat related CWR did not have any threatened category since there are plenty of them are conserved in gene banks and ex situ. Moreover, there are some of them are assigned as Data Deficient, therefore, more detailed information about their population and threats are needed.

5.7. CONCLUSION

A total of 88 CWR taxa were red list assessed, 47% of them were assessed as Least Concern (41 taxa), 28 % of the total were assessed as Near Threatened (25 taxa), 21% as Data Deficient (18 taxa), 3% as Endangered (three taxa) and 1% as Critically Endangered (One taxa).

The recommendation is to conserve the taxa that are more threatened such as *(Medicago halophila* - (Boiss.) E.Small*)* which was assessed as Critically Endangered.

Then to conserve the three taxa that were assessed as Endangered; those are *Cicer bijugum* Rech.f., *Medicago crassipes* - (Boiss.) E.Small, and *Medicago cretacea* - M. Bieb.

Some CWR are assessed as Data Deficient, therefore, there is an urgent need to complete the data related to their distribution, population and threats. It is important to monitor the status of the taxa that were assessed as Near Threatened as intensive farming, urbanisation, grazing and climate change are disturbing these taxa natural habitat causing a future decline in their population.

5. CHAPTER 6: AN OVERALL SYNTHESIS TO THE THESIS

Conservation of crop wild relatives' diversity in the Fertile Crescent: a strategy for conservation and future utilisation

A scientific approach to the conservation of crop wild relatives was displayed in this thesis in general and for the Fertile Crescent in particular. The aim is to conserve CWRs in the region to meet the targets set out by the Convention on Biological Diversity (CBD, 1992), which outlined the need to conserve plant genetic resources. In addition, CWR are threatened in their natural environment in the Fertile Crescent due to several factors including infrastructure and building, pollution, soil erosion, overgrazing, and agriculture intensification (El-Beltagy, 2006; Derneg, 2010). Climate change has also impacted on the vegetation in the Fertile Crescent (Trigo *et al.*, 2010). To conserve plant genetic resources in the Fertile Crescent is vital, not only because the Fertile Crescent has two Vavilov centers (Vavilov, 1926) but also early farming started in Southwest Asia (the Fertile Crescent today) (Willcox, 2012) and also the Fertile Crescent is a centre for domestication of nine major crops including einkorn, emmer, barley, lentil, pea, chickpea, bitter vetch, broad bean, flax (Willcox, 2012). In addition, the Fertile Crescent is one of the regions with the highest concentration of CWR per unit area globally (Vincent *et al.*, 2013). One of the most significant regions for safeguarding global food security is the Fertile Crescent and only a few studies have been carried out on CWR in the Fertile Crescent (Keisa *et al.*, 2008). Keisa *et al*. (2008) indicated the need to use modern genetic and GIS technologies to develop a regional strategy for CWR conservation for the Fertile Crescent and consequently help in guarding global food security. The overarching goal of the thesis is set out as being to analyse the biodiversity of the major representative crops and their crop wild relatives (CWR) in the Fertile Crescent and the development of a systematic CWR strategy as an aid to underpinning global food security. There was a logical progression of work moving from plant diversity section which gave an insight to why the Fertile Crescent has been chosen in this study as it is as part of the Mediterranean Basin and stands within the top 15 hotspots for plant biodiversity. The Fertile Crescent interdictory sector gave an insight that it is a centre for domestication of major crops including barley, einkorn wheat, oat, and rye. The subecoregion section and map in the Fertile Crescent display an overview of different environmental zones in the Fertile

Crescent and this gave a clearer picture to where CWR are distributed. The Fertile Crescent plate map displays future threats to CWR by plate movements (earthquakes). The geography of the Fertile Crescent study provides information on mountains, rivers, climate, soil, and this information are vital to helping in conserving CWR as well as providing insight on the distribution as distribution depends on altitude, soil type, and rain. The history and origin of the Fertile Crescent section provided an insight that agriculture was first started in the Fertile Crescent. The study provided the number of endemic plants in the Fertile Crescent. The agriculture biodiversity study revealed that the Fertile Crescent contains two centres of origin the first centre is the Asia Minor and Mediterranean which include a large diversity of crop gene pool. The first step toward developing a regional conservation strategy for CWR is to establish the CWR priority list (Magos Brehm *et al.*, 2010). The species approach was applied as opposed to the ecological approach. As crop wild relatives are neglected in their natural environmental conditions where they face various threats, displaying a CWR priority list on a map has been always a desire by the scientific community and this was systematically achieved in this study. The data on the Eco social value of crops was vital to the prioritisation study as it presented energy supply, fat supply protein supply of CWR related crops which are major prioritisation criteria. Climate change in the Fertile Crescent literature review indicates that climate change is happening in the Fertile Crescent at an alarming rate as annual surface temperature has increased over the years and continues to increase, and this justifies why it was necessary to conduct an assessment of the climate change impact on CWR in the Fertile Crescent. The conservation of agriculture biodiversity sections gave an insight into the type of conservation available for CWR (*in situ* and *ex situ*). It was also important to display protected areas in the Fertile Crescent as this was used later in the gap analysis section. The chapter then discussed CWR in general and why they are vital to food security. The study went on to achieve its goals and objectives by compiling a checklist of CWR for the Fertile Crescent through prioritisation, gap analysis, complementary analysis and the identification of potential sites for *in-situ* conservation and the potential effect of climate change and IUCN Red Listing.

6.1. KEY FINDINGS

The work completed in this study resulted in the following findings.

1. Passport data of CWR that include occurrence records in a clean and tidy format was provided for the Fertile Crescent. Information gaps were filled and duplications were removed (Chapter 2).

2. The inventory of 220 priority CWR for the Fertile Crescent provides a well-focused list that needs conservation the most. Since the financial resources to conserve all the CWR are limited and accordingly, such inventory helps to improve the *in-situ* and *ex-situ* conservation and the genetic diversity of CWR. The methods used in prioritisation took into account previously used methods and used innovative new methods that can be applied in setting national, regional, and global conservation strategies.

3. A regional database of occurrence records has been created for CWR priority list for the Fertile Crescent.

4. The richest hotspots of CWR diversity have been identified in the Fertile Crescent and are located in Syria near the Lebanese border and the Syrian Coastal Mountain Range in north-western Syria, north western Jordan and several places in Turkey.

5. Ten virtual CWR genetic reserves have been recommended for the Fertile Crescent. Both data and methodology applied can be used in setting strategies to conserve CWR plant genetic resources.

6. The *ex-situ* gap examination has shown that 30% of CWR species have no representation in gene banks and 70% of the CWR examined species are represented.

7. Significant gaps in *ex-situ* conservation occur in the west and south of Turkey across the Mediterranean Seashore, North Lebanon, and west of Syria (in Latakia and Tartus Governorate), across the border between Turkey and Syria and northern Iraq.

8. *Aegilops bicornis* and *Triticum monococcum*, a wild relative of wheat, are expected to be highly impacted by climate change, as their potential distribution areas were estimated to be reduced by 31 (%). Moreover, the dispersal of *T. monococcum* is predicted to move toward the north as newly suitable areas are likely to be available in northern Iraq. *Cicer bijugum,* a wild relative of chickpea, *Vicia grandiflora,* and *Beta corolliflora* are expected to be slightly impacted by climate change, as their potential distribution areas were estimated to be reduced by 4 (%).

9. Several CWR taxa (88) were red list assessed based on the IUCN criteria and categories and 47% of the total taxa that was assessed are Least Concern. Around

28 % of them are Near Threatened. Data Deficient accounted for 21% of the taxa and 3% were assessed as Endangered (three taxa). One percent were assessed as Critically Endangered (One taxa).

6.2. LIMITATIONS

The species distribution modelling showed provides it is accurate and is sufficient to undertake such study for the Fertile Crescent region. Analysis for each country individually can be done by choosing different parameters. Obtaining digital hotspots of CWR is vital as it saves a lot of time looking for these taxa. It allows easy access to CWR so scientists can visit such sites and collect samples for using in a gene transfer or breeding programme as well as other scientific use. It also allows the staff of gene banks to collect seeds for *ex-situ* conservation. Occurrence records and passport data are constantly updated and improved on a daily basis. The species distribution modelling depends greatly on the quality of the data used to undertake such analysis. Therefore, the output of the species distribution modelling varies according to the data used. The result presented here is as a result of the data available at the time of the study and this is likely to slightly differ if more occurrence records are collected. In addition, species distribution range is likely to change as a result of climate change and new occurrence records will be updated which may change the richness map.

The contradictory taxonomic classification and synonym for the same taxon was another issue. This study tries to address some taxonomic classification issues and therefore a new list of CWR priority list with accurate taxonomic classification has been achieved in the gap analysis section. For the climate change section, the result is based on the current and future climate change scenario. However, other factors are not presented here such as abiotic and biotic interfere with climate change which also impacts on the distribution of plant genetic materials. Species' migration ability has been addressed in the climate change section. In addition, other factors have not been assessed since the Fertile Crescent is experiencing war where weapons of mass destruction were used, and this impacted on the distribution of CWR and conservation work and initiatives.

The IUCN Red List assessment is a very useful tool in putting CWR in different categories and allowing them to be used in prioritisation for conservation since the endangered ones have a priority over those of least concern.

Although the work presented here analyses the diversity of major CWR in the Fertile Crescent, more work should be done using molecular markers to assess the genetic diversity. Although some regions are labelled as a war zone and cannot be entered, it is important to collect fresh samples of CWR plant genetic materials, as this will help in the conservation of CWR *ex situ* and *in situ* and to perfect the result of the gap analysis.

6.3. FUTURE WORK

Based on this CWR list, molecular analysis can be utilised to investigate the structure of these CWR and to find potential gene donors as well as to find underrepresented taxa in gene banks. A lot of these CWR taxa still lack data regarding their morphology, population size and threats. Filling the data gap can be achieved through using molecular analysis as well as field visits and population size identifications.

More drought and temperature variation tolerance should be investigated for these CWR either in the lab or by field trails, so these CWR can be used in breeding programmes and can enhance current cultivated crop varieties.

An updated assessment of the threats to CWR in the Fertile Crescent is required. Threats to CWR is a dynamic concept that keep changing over time. Therefore, it is worth updating the threat assessment periodically.

More collaboration between different disciplines is needed to link these CWR and their good genes with their future use in agriculture and to improve yield. The collaboration should be done with gene banks, agriculture research centres, botanic gardens, and seed companies.

The conservation strategy outlined in this research should be implemented by governmental bodies and research institutions.

Genetic diversity analysis should be performed frequently through the use of accessible molecular markers related to adaptive traits and by collecting more occurrence records and passport data. Re-prioritisation and gap analysis should be frequently undertaken to ensure effective implementation of both the *in-situ* and *ex-situ* conservation.

It should also be ensured that CWR in protected areas are conserved adequately and are available for plant breeders and research institutions to use.

6.4. CONCLUSION

A checklist of CWR was created for the Fertile Crescent containing 21,080 taxa. A total of 835 of these taxa are CWR that are related to crops which have socio-economic value in the region. A regional CWR priority list containing 220 CWR taxa was created for the CWR checklist based on 12 prioritisation criteria. A new CWR priority list containing 441 CWR taxa was re-established based on recent published data sources. The priority list is used in the gap analysis section. A total of 23,878 presence points representing 441 CWR priority list species in the Fertile Crescent were collated and used in the gap analysis.

The occurrence records and passport data for each taxon allowed establishment of a richness map for CWR in the region. The richest hotspots for CWR diversity have been identified and are located in Syria near the Lebanese border and the Syrian Coastal Mountain Range in north-western Syria, north-western Jordan and several places in Turkey.

The richness map allowed the establishment of 10 sites recommended for establishing CWR genetic reserves. The first site is in Syria in Tel Kalakh. The second site is in Turkey in Menemen. The third site is in Turkey in Burc Karakuyu. The fourth site is in Turkey in Cankaya. The fifth site is in Turkey in Siverek. The sixth site is in Turkey in Kumkale Koyu. The seventh site is in Palestinian in Anata. The eighth site is in Turkey in Anamur. The ninth site is in Turkey in Doyran. The tenth site is in Turkey in Tebrizcik. Such genetic reserves will allow for the utilisation of CWR genetic materials for plant breading and research and development use.

A complementarity analysis using CAPFITOGEN has also been performed and it was discovered that the top sites with the highest CWR taxa concentration are found in eastern Turkey with two blue grid squares containing at least 36 CWR taxa each. The next highest CWR taxa is found in north-east Turkey, not far from the first two. The fourth highest CWR taxa is found in Latakia in Syria with the light blue square containing 20-35 CWR taxa. The fives, sixth, seventh highest CWR taxa are found in Turkey with the yellow square containing 9-20 CWR taxa, one in Izmir Province, one in Kumluca Antalya, and one in the South-eastern Anatolia Region near Diyarbakır.

The *ex-situ* conservation gap analysis analysed the current representation in gene banks of CWR and found out that 30% of CWR species have no representation

in gene banks and 70% of the CWR examined species are represented. Therefore, collection is needed for those underrepresented ones. Significant gaps in *ex-situ* conservation occur in the west and south of Turkey across the Mediterranean seashore, North Lebanon, and west of Syria (in Lattakia and Tartus Governorate), across the border between Turkey and Syria, and Northern Iraq.

The climate change section revealed that *Aegilops bicornis*, a wild relative of bread wheat, and *Triticum monococcum*, a wild relative of wheat, are expected to be highly impacted by climate change. Moreover, the dispersal of *T. monococcum* is predicted to move toward the north as new suitable areas are likely to be available in northern Iraq. *Cicer bijugum*, a wild relative of chickpea, *Vicia grandiflora*, a wild relative of common vetch, and *Beta corolliflora*, a wild relative of sugar beet, are expected to be slightly impacted by climate change, as their potential distribution areas were estimated to be reduced. Therefore, taxa that are impacted by climate change and their distribution range will be restricted, thus creating a conservation action plan for those taxa highly impacted.

A total of 88 CWR taxa were red list assessed, 47% of them were assessed as Least Concern (41 taxa), 28 % of the total were assessed as Near Threatened (25 taxa), 21% as Data Deficient (18 taxa), 3% as Endangered (three taxa) and 1% as Critically Endangered (One taxa).

The *in-situ* and *ex-situ* conservation ensure that CWR genetic materials are readily available for plant breeders and the scientific community to use either to transfer desirable genes to cultivated crops or to conduct further research such as on CWR genetic behaviour and their adaptation to different environmental conditions and temperature variation in the case of climate change. In addition, CWR genetic materials will be accessible in the event of natural disasters such as earthquakes, volcanos, tsunamis, tornados, erosion, desertification, and other natural disasters.

CWR will also be available during manmade disasters such as wars, pollution, nuclear power plants leakage and atomic radiations, contamination from biological weapon leakage and contamination with toxic chemical substances.

In addition, it is likely that CWR genetic materials will also be available for space missions use. Since Hopkins states that humans need to find an alternative planet in space as the natural resources on Earth are limited and overpopulation puts more

pressure on our natural recourses, there is a possibility that plant genetic materials will be used to help make planets more inhabitable by humans and to assist in the reclamation process of some planets' soil. CWR will be also likely to be used as a source of food in space exploration missions, and one of them is likely to be on Mars due to CWR adaptability.

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Supplementary material 1, the R script used to run the complementarity analysis

```
ruta<-"E:/CAPFITOGEN2"
#Dataset original form Wathek
#pasaporte<-"Wathek/WathekTableGEOQUAL_final.txt"
#Datasets adjusted for only the target countries or countries with PA maps
#pasaporte<-"Wathek/Points1_WithinTargetCountries1.txt"
pasaporte<-"Wathek/Points2_WithinCountriesWithPA1.txt"
geoqual<-TRUE
totalqual<-50
gaptype<-FALSE
gaptresh<-5
gapna<-"include"
duplicat<-TRUE
distdup<-1
celdas<-TRUE
resol1<-"celdas 10x10 km aprox (5 arc-min)"
#resol1<-"Celdas 5x5 km aprox (2.5 arc-min)"
nceldas<-10
areas<-TRUE
WDPA<-TRUE
#pais<-"Albania"
#WDPA layers for countries with PA maps, in this case "Armenia" is in fact the set of PA for Iraq, Jordan, Lebanon, Israel, Palestina and Cyprus (excluding Turkey, Syria and NOrthenr Cyprus)
pais<-"Armenia"
#WDPA layers for all the target countries, in this case "Syria" is in fact the set of PA for Turkey, Iraq, Jordan, Lebanon, Israel, Palestina and Cyprus.
#pais<-"Syria"
propio<-FALSE
nombre<-"NA"
campo<-"NA"
nareas<-10
```

```
coveran<-TRUE
niveltax<-"species"
datanatax<-FALSE
mapaelcf<-FALSE
mapaelc<-"NA"
datanaelc<-FALSE
data0elc<-FALSE
#resultados<-"E:/CAPFITOGEN2/ResultadosWathek/ComplementaAllDataSet"
#resultados<-"E:/CAPFITOGEN2/ResultadosWathek/ComplementaTargetCountries"
resultados<-"E:/CAPFITOGEN2/ResultadosWathek/ComplementaCountriesPA"
#########################################################################
###
# Script herramienta Complementa
# Esta es una herramienta para la identificación de áreas complementarias
# para la conservación in situ de los recursos fitogenéticos
# Autor de la herramienta: Mauricio Parra Quijano,
# mauricio.parra@fao.org, Programa CAPFITOGEN, http://capfitogen.net
# Tratado Internacional sobre los Recursos Fitogeneticos
# para la Alimentacion y la Agricultura 2015
#########################################################################
###
#You can freely use and modify this script only for non-commercial purposes.Otherwise please contact to script author.
#In any case, we encourage you include in your study publication the correspondent credits (about R software, packages and script author).
#Citation: Parra-Quijano, M., Torres, E., Iriondo, J.M. and López, F. 2014. CAPFITOGEN Tools User Manual Version 1.2. International Treaty on Plant Genetic Resources for Food and Agriculture, FAO, Rome, Italy. 138p. ISBN 978-92-5-108493-9
#########################################################################
########################################
```

```
#############################################################################
########################################
##Parámetros
setwd(paste(resultados))
write(paste(), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write("_____",
file="Parametros.Parameters.Complementa.txt", append=TRUE)
write("_____Herramienta/Tool Complementa_____",
file="Parametros.Parameters.Complementa.txt", append=TRUE)
write("_____",
file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("Lista de parametros usados en: ", date(),sep=""),
file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("List of parameters used on: ", date(),sep=""),
file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste(), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("ruta:", ruta,sep=""), file="Parametros.Parameters.Complementa.txt",
append=TRUE)
write(paste("pasaporte:", pasaporte,sep=""),
file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("geoqual:", geoqual,sep=""),
file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("totalqual:", totalqual,sep=""),
file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("gaptype:", gaptype,sep=""),
file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("gaptresh:", gaptresh,sep=""),
file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("gapna:", gapna,sep=""), file="Parametros.Parameters.Complementa.txt",
append=TRUE)
write(paste("duplicat:", duplicat,sep=""),
file="Parametros.Parameters.Complementa.txt", append=TRUE)
```

```
write(paste("distdup:", distdup,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("celdas:", celdas,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("resol1:", resol1,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("nceldas:", nceldas,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("areas:", areas,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("WDPA:", WDPA,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("pais:", pais,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("propio:", propio,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("nombre:", nombre,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("campo:", campo,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("nareas:", nareas,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("coveran:", coveran,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("niveltax:", niveltax,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("datanatax:", datanatax,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("mapaelcf:", mapaelcf,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("mapaelc:", mapaelc,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
```

```
write(paste("datanaelc:", datanaelc,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("data0elc:", data0elc,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
write(paste("resultados:", resultados,sep=""), file="Parametros.Parameters.Complementa.txt", append=TRUE)
##Elemento introducido por el usuario: ruta (ext)
#Determinar esa ruta como directorio de trabajo
setwd(paste(ruta))
#Paquetes a cargar
library(sp)
library(raster)
library(maptools)
library(rgeos)
pasaporte<-read.delim(paste("Pasaporte/",pasaporte,sep=""))
#Trifurcación (sin coordenadas, con coordenadas sexagesimales, con coordenadas decimales)
sexagesimal<-subset(pasaporte,(!is.na(LATITUDE)&!is.na(LONGITUDE)))
sexagesimal<-sexagesimal[,c(1:22,24,26:ncol(sexagesimal))]
decimal<-
subset(pasaporte,(is.na(LATITUDE)|is.na(LONGITUDE))&(!is.na(DECLATITUDE)&!is.na(DECLONGITUDE)))
###Sexagesimal a decimal
#Obtención de las coordenadas en formato decimal a partir de sexagesimal codificadas tal como lo indica el formato IPGRI 2001
if(length(sexagesimal[,1])>0){
  coordec<-as.data.frame(matrix(nrow = length(sexagesimal[,1]), ncol = 2))
  #colnames(coordec)[1]<-"DECLATITUDE"
  #colnames(coordec)[2]<-"DECLONGITUDE"
  coordec<-data.frame(sexagesimal$ACCENUMB,coordec)
  colnames(coordec)[1]<-"ACCENUMB"
  for (i in 1:length(sexagesimal[,1])) {
```

```
    coordec[i,2]<-ifelse(sexagesimal$LATITUDE[i]=='NA','NA',
((as.numeric(substr(sexagesimal$LATITUDE[i],1,2))+
(ifelse(substr(sexagesimal$LATITUDE[i],3,4)=='--
',0,(as.numeric(substr(sexagesimal$LATITUDE[i],3,4))/60)))+
 (ifelse(substr(sexagesimal$LATITUDE[i],5,6)=='--
',0,(as.numeric(substr(sexagesimal$LATITUDE[i],5,6))/3600))))
*(as.numeric(ifelse(substr(sexagesimal$LATITUDE[i],7,7)=='N',1,-1)))))
    coordec[i,3]<-ifelse(sexagesimal$LONGITUDE[i]=='NA','NA',
((as.numeric(substr(sexagesimal$LONGITUDE[i],1,3))+

(ifelse(substr(sexagesimal$LONGITUDE[i],4,5)=='--
',0,(as.numeric(substr(sexagesimal$LONGITUDE[i],4,5))/60)))+

(ifelse(substr(sexagesimal$LONGITUDE[i],6,7)=='--
',0,(as.numeric(substr(sexagesimal$LONGITUDE[i],6,7))/3600))))

*(as.numeric(ifelse(substr(sexagesimal$LONGITUDE[i],8,8)=='E',1,-1)))))
  }
  sexagesimal<-
cbind(sexagesimal[,1:22],coordec[,2],sexagesimal[,23],coordec[,3],sexagesimal[,24:
ncol(sexagesimal)])
  colnames(sexagesimal)[23]<-"DECLATITUDE"
  colnames(sexagesimal)[24]<-"LATITUDE"
  colnames(sexagesimal)[25]<-"DECLONGITUDE"
  write("5.Terminado proceso de transformación sexagesimal a decimal",
file="Error/process_info.txt", append=TRUE)
  ###Unificación coordenadas sexagesimal a decimal y decimal original
  puntosorig<-rbind(sexagesimal,decimal)
}
if(length(sexagesimal[,1])==0){
  puntosorig<-decimal
}
```

```
####################
#Filtros
#Por GEOQUAL
if(geoqual){
  puntosorig<-subset(puntosorig,TOTALQUAL100>=paste(totalqual))
}
#Por tipo de gap (de Representa)
if(gaptype){
  if(gapna=="include"){
    puntosorigA<-subset(puntosorig,GAPTYPE<gaptresh)
    puntosorigB<-subset(puntosorig,is.na(GAPTYPE))
    puntosorig<-rbind(puntosorigA,puntosorigB)
  }
  if(gapna=="exclude"){
    puntosorig<-subset(puntosorig,GAPTYPE<gaptresh)
  }
}

##Extracción de categoría ELC si fuera necesaria
if(mapaelcf){
  namespas<-colnames(puntosorig)
  if(any(namespas=="BG_ELC")){
    if(is.na(unique(puntosorig$BG_ELC))){
      mapaelc<-raster(paste("ELCmapas/",mapaelc,sep=""))
      puntosBG<-
SpatialPoints(puntosorig[,c("DECLONGITUDE","DECLATITUDE")],proj4string=CRS(
"+proj=longlat +datum=WGS84 +ellps=WGS84 +towgs84=0,0,0"))
      BGcat<-extract(mapaelc,puntosBG)
      puntosorig$BG_ELC<-BGcat
    }
  }
  if(!any(namespas=="BG_ELC")){
```

```
    mapaelc<-raster(paste("ELCmapas/",mapaelc,sep=""))
    puntosBG<-
SpatialPoints(puntosorig[,c("DECLONGITUDE","DECLATITUDE")],proj4string=CRS(
"+proj=longlat +datum=WGS84 +ellps=WGS84 +towgs84=0,0,0"))
    BG_ELC<-extract(mapaelc,puntosBG)
    puntosorig<-cbind(puntosorig,BG_ELC)
  }
}
#Simplificación de tabla

if(geoqual&gaptype){
  puntosorig<-
data.frame(puntosorig$ACCENUMB,puntosorig$GENUS,puntosorig$SPECIES,punt
osorig$SUBTAXA,puntosorig$DECLATITUDE,puntosorig$DECLONGITUDE,puntos
orig$TOTALQUAL100,puntosorig$BG_ELC,puntosorig$GAPTYPE)
  colnames(puntosorig)[1]<-"ACCENUMB"
  colnames(puntosorig)[2]<-"GENUS"
  colnames(puntosorig)[3]<-"SPECIES"
  colnames(puntosorig)[4]<-"SUBTAXA"
  colnames(puntosorig)[5]<-"DECLATITUDE"
  colnames(puntosorig)[6]<-"DECLONGITUDE"
  colnames(puntosorig)[7]<-"TOTALQUAL100"
  colnames(puntosorig)[8]<-"BG_ELC"
  colnames(puntosorig)[9]<-"GAPTYPE"
}
if(geoqual&!gaptype){
  puntosorig<-
data.frame(puntosorig$ACCENUMB,puntosorig$GENUS,puntosorig$SPECIES,punt
osorig$SUBTAXA,puntosorig$DECLATITUDE,puntosorig$DECLONGITUDE,puntos
orig$TOTALQUAL100,puntosorig$BG_ELC)
  colnames(puntosorig)[1]<-"ACCENUMB"
  colnames(puntosorig)[2]<-"GENUS"
```

```
  colnames(puntosorig)[3]<-"SPECIES"
  colnames(puntosorig)[4]<-"SUBTAXA"
  colnames(puntosorig)[5]<-"DECLATITUDE"
  colnames(puntosorig)[6]<-"DECLONGITUDE"
  colnames(puntosorig)[7]<-"TOTALQUAL100"
  colnames(puntosorig)[8]<-"BG_ELC"
}
if(!geoqual&gaptype){
  puntosorig<-
data.frame(puntosorig$ACCENUMB,puntosorig$GENUS,puntosorig$SPECIES,punt
osorig$SUBTAXA,puntosorig$DECLATITUDE,puntosorig$DECLONGITUDE,puntos
orig$BG_ELC,puntosorig$GAPTYPE)
  colnames(puntosorig)[1]<-"ACCENUMB"
  colnames(puntosorig)[2]<-"GENUS"
  colnames(puntosorig)[3]<-"SPECIES"
  colnames(puntosorig)[4]<-"SUBTAXA"
  colnames(puntosorig)[5]<-"DECLATITUDE"
  colnames(puntosorig)[6]<-"DECLONGITUDE"
  colnames(puntosorig)[7]<-"BG_ELC"
  colnames(puntosorig)[8]<-"GAPTYPE"
}
if(!geoqual&!gaptype){
  puntosorig<-
data.frame(puntosorig$ACCENUMB,puntosorig$GENUS,puntosorig$SPECIES,punt
osorig$SUBTAXA,puntosorig$DECLATITUDE,puntosorig$DECLONGITUDE,puntos
orig$BG_ELC)
  colnames(puntosorig)[1]<-"ACCENUMB"
  colnames(puntosorig)[2]<-"GENUS"
  colnames(puntosorig)[3]<-"SPECIES"
  colnames(puntosorig)[4]<-"SUBTAXA"
  colnames(puntosorig)[5]<-"DECLATITUDE"
  colnames(puntosorig)[6]<-"DECLONGITUDE"
```

```
  colnames(puntosorig)[7]<-"BG_ELC"
}
#Concatenación y exclusión o no de valores taxonómicos/ecogeográficos NA
if(niveltax=="genus"){
  CHAIN<-vector(mode = "character", length = length(puntosorig[,1]))
  if(datanatax){
    if(mapaelcf){
      for(i in 1:length(puntosorig[,1])){
        CHAIN[i]<-paste(puntosorig$GENUS[i],puntosorig$BG_ELC[i],sep="_")
      }
      puntosorig<-cbind(puntosorig,CHAIN)
      if(!data0elc){
        puntosorig<-subset(puntosorig, BG_ELC!=0)
      }
      if(!datanaelc){
        puntosorig<-subset(puntosorig,!is.na(BG_ELC))
      }
    }
    if(!mapaelcf){
      for(i in 1:length(puntosorig[,1])){
        CHAIN[i]<-paste(puntosorig$GENUS[i])
      }
      puntosorig<-cbind(puntosorig,CHAIN)
    }
  }
  if(!datanatax){
    if(mapaelcf){
      for(i in 1:length(puntosorig[,1])){
        CHAIN[i]<-paste(puntosorig$GENUS[i],puntosorig$BG_ELC[i],sep="_")
      }
      puntosorig<-cbind(puntosorig,CHAIN)
      if(!data0elc){
```

```
      puntosorig<-subset(puntosorig, BG_ELC!=0)
    }
    if(!datanaelc){
      puntosorig<-subset(puntosorig,!is.na(BG_ELC))
    }
  }
  if(!mapaelcf){
    for(i in 1:length(puntosorig[,1])){
      CHAIN[i]<-paste(puntosorig$GENUS[i])
    }
    puntosorig<-cbind(puntosorig,CHAIN)
  }
  puntosorig<-subset(puntosorig, !is.na(GENUS))
 }
}
if(niveltax=="species"){
 CHAIN<-vector(mode = "character", length = length(puntosorig[,1]))
 if(datanatax){
  if(mapaelcf){
    for(i in 1:length(puntosorig[,1])){
      CHAIN[i]<-
paste(puntosorig$GENUS[i],puntosorig$SPECIES[i],puntosorig$BG_ELC[i],sep="_")
    }
    puntosorig<-cbind(puntosorig,CHAIN)
    if(!data0elc){
      puntosorig<-subset(puntosorig, BG_ELC!=0)
    }
    if(!datanaelc){
      puntosorig<-subset(puntosorig,!is.na(BG_ELC))
    }
  }
  if(!mapaelcf){
```

```
      for(i in 1:length(puntosorig[,1])){
        CHAIN[i]<-paste(puntosorig$GENUS[i],puntosorig$SPECIES[i],sep="_")
      }
      puntosorig<-cbind(puntosorig,CHAIN)
    }
  }
  if(!datanatax){
    if(mapaelcf){
      for(i in 1:length(puntosorig[,1])){
        CHAIN[i]<-
paste(puntosorig$GENUS[i],puntosorig$SPECIES[i],puntosorig$BG_ELC[i],sep="_")
      }
      puntosorig<-cbind(puntosorig,CHAIN)
      if(!data0elc){
        puntosorig<-subset(puntosorig, BG_ELC!=0)
      }
      if(!datanaelc){
        puntosorig<-subset(puntosorig,!is.na(BG_ELC))
      }
    }
    if(!mapaelcf){
      for(i in 1:length(puntosorig[,1])){
        CHAIN[i]<-paste(puntosorig$GENUS[i],puntosorig$SPECIES[i],sep="_")
      }
      puntosorig<-cbind(puntosorig,CHAIN)
    }
    puntosorig<-subset(puntosorig, !is.na(SPECIES))
  }
}

if(niveltax=="subtaxa"){
  CHAIN<-vector(mode = "character", length = length(puntosorig[,1]))
```

```
  if(datanatax){
    if(mapaelcf){
      for(i in 1:length(puntosorig[,1])){
        CHAIN[i]<-
paste(puntosorig$GENUS[i],puntosorig$SPECIES[i],puntosorig$SUBTAXA[i],puntos
orig$BG_ELC[i],sep="_")
      }
      puntosorig<-cbind(puntosorig,CHAIN)
      if(!data0elc){
        puntosorig<-subset(puntosorig, BG_ELC!=0)
      }
      if(!datanaelc){
        puntosorig<-subset(puntosorig,!is.na(BG_ELC))
      }
    }
    if(!mapaelcf){
      for(i in 1:length(puntosorig[,1])){
        CHAIN[i]<-
paste(puntosorig$GENUS[i],puntosorig$SPECIES[i],puntosorig$SUBTAXA[i],sep="_
")
      }
      puntosorig<-cbind(puntosorig,CHAIN)
    }
  }
  if(!datanatax){
    if(mapaelcf){
      for(i in 1:length(puntosorig[,1])){
        CHAIN[i]<-
paste(puntosorig$GENUS[i],puntosorig$SPECIES[i],puntosorig$SUBTAXA[i],puntos
orig$BG_ELC[i],sep="_")
      }
      puntosorig<-cbind(puntosorig,CHAIN)
```

```
      if(!data0elc){
        puntosorig<-subset(puntosorig, BG_ELC!=0)
      }
      if(!datanaelc){
        puntosorig<-subset(puntosorig,!is.na(BG_ELC))
      }
    }
    if(!mapaelcf){
      for(i in 1:length(puntosorig[,1])){
        CHAIN[i]<-
paste(puntosorig$GENUS[i],puntosorig$SPECIES[i],puntosorig$SUBTAXA[i],sep="_
")
      }
      puntosorig<-cbind(puntosorig,CHAIN)
    }
    puntosorig<-subset(puntosorig, !is.na(SUBTAXA))
  }
}
#
#Eliminación de duplicados espaciales por taxa o taxa-eu
if(duplicat){
  taxaN<-unique(puntosorig$CHAIN)
  puntosor<-list()
  for (i in 1:length(taxaN)){
    puntosro1<-subset(puntosorig,CHAIN==taxaN[i])
    puntosdistdup<-
SpatialPointsDataFrame(puntosro1[,c("DECLONGITUDE","DECLATITUDE")],puntos
ro1,proj4string=CRS("+proj=longlat +datum=WGS84 +ellps=WGS84
+towgs84=0,0,0"))
    if (mean(puntosro1$DECLATITUDE)<23){
      distdup1<-distdup*0.00833
    }
```

```
    if (mean(puntosro1$DECLATITUDE)>23&mean(puntosro1$DECLATITUDE)<45){
      distdup1<-distdup*0.00975
    }
    if (mean(puntosro1$DECLATITUDE)>45&mean(puntosro1$DECLATITUDE)<67){
      distdup1<-distdup*0.0127
    }
    if (mean(puntosro1$DECLATITUDE)>67){
      distdup1<-distdup*0.02299
    }
    puntosdistdup<-remove.duplicates(puntosdistdup,zero=distdup1)
    puntosor[[i]]<-puntosdistdup@data
  }
  rm(taxaN)
  rm(puntosro1)
  rm(puntosdistdup)
  puntosorig<-do.call("rbind",puntosor)
  rm(puntosor)
}

#####################################################################
#####################################################################
#Análisis por Celda
#####################################################################
if(celdas){
  #creación directorio para análisis de celdas
  setwd(paste(resultados))
  dir.create(as.vector(paste("AnalisisCeldas_CellAnalysis")))
  resultadosCell<-paste(resultados,"/AnalisisCeldas_CellAnalysis",sep="")
  setwd(paste(ruta))
  #Carga de resoluciones
  load("resol.RData")
  resol<-subset(resol,resolucion==paste(resol1))
```

```
  resol<-resol[1,3]

  #puntos espaciales sin dataframe
  puntos<-SpatialPoints(puntosorig[,c(6,5)])

  #Creación Raster base
  xmin<-min(puntosorig$DECLONGITUDE)-resol
  xmax<-max(puntosorig$DECLONGITUDE)+resol
  ymin<-min(puntosorig$DECLATITUDE)-resol
  ymax<-max(puntosorig$DECLATITUDE)+resol
  extension<-extent(xmin,xmax,ymin,ymax)
  aaa<-raster(extension)
  res(aaa)<-resol
  aaa<-rasterFromCells(aaa, 1:ncell(aaa))

  #extraccion cell value
  cellvalue<-extract(aaa,puntos)
  puntosorig<-cbind(puntosorig,cellvalue)
  puntosfuera<-subset(puntosorig,is.na(cellvalue))
  if(nrow(puntosfuera)>0){
    puntosfuera<-SpatialPointsDataFrame(puntosfuera[,c(6,5)],puntosfuera)
    writePointsShape(puntosfuera,paste(resultadosCell,"/points_out_grid",sep=""))
  }
  puntosorig<-subset(puntosorig,!is.na(cellvalue))
  puntosorigshp<-SpatialPointsDataFrame(puntosorig[,c(6,5)],puntosorig)

writePointsShape(puntosorigshp,paste(resultadosCell,"/final_analyzed_points",sep="
"))

  ###Armado de tabla para Rebelo
  #lista de valores de celda mapa molde
  columnas<-unique(puntosorig$cellvalue)
```

```
  #lista genus-especies-subsp-elc
  filas<-unique(puntosorig$CHAIN)
  #Armazón
  tablafin<-matrix(data=0,nrow=length(filas),ncol=length(columnas))
  colnames(tablafin)<-columnas
  rownames(tablafin)<-filas
  for(i in 1:length(filas)){
    tabla1<-subset(puntosorig,puntosorig$CHAIN==paste(filas[i]))
    tabla1<-unique(tabla1$cellvalue)
    for (j in 1:length(columnas)){
      if(any(tabla1==colnames(tablafin)[j])){
        tablafin[i,j]<-1
      }
    }
  }
  #Se salva la tabla
  tablafin2<-cbind(as.character(filas),tablafin)
  colnames(tablafin2)[1]<-"Genus_Sp_Subtaxa_ELC"
  write.table(tablafin2,paste(resultadosCell,"/Tabla_Table_Base.txt",sep=""),    sep    =
"\t", row.names = FALSE, col.names=TRUE, qmethod = "double")
  write.table(tablafin2,paste(resultadosCell,"/Tabla_Table_Base.xls",sep=""),    sep    =
"\t", row.names = FALSE, col.names=TRUE, qmethod = "double")
  ######################
  #Tablas estadísticas totales (sin eliminar por complementariedad)
  #por celdas
  suma_sum<- data.frame(apply(tablafin, 2, sum))
  suma_sum<-data.frame(rownames(suma_sum),suma_sum)
  colnames(suma_sum)[1]<-"CELL_ID"
  colnames(suma_sum)[2]<-"N_Dif_Taxa_ELC"

write.table(suma_sum,paste(resultadosCell,"/Datos_por_Celda_Data_by_CELL.txt",
sep=""), sep = "\t", row.names = FALSE, col.names=TRUE, qmethod = "double")
```

```
write.table(suma_sum,paste(resultadosCell,"/Datos_por_Celda_Data_by_CELL.xls",
sep=""), sep = "\t", row.names = FALSE, col.names=TRUE, qmethod = "double")
  #Por Especie
  suma_sum1<- data.frame(apply(tablafin, 1, sum))
  suma_sum1<-data.frame(rownames(suma_sum1),suma_sum1)
  colnames(suma_sum1)[1]<-"Taxon_ID_ELC"
  colnames(suma_sum1)[2]<-"N_Pops_in_CELLS"

write.table(suma_sum1,paste(resultadosCell,"/Datos_por_Taxa_ELC_Data_by_Taxa
_ELC.txt",sep=""), sep = "\t", row.names = FALSE, col.names=TRUE, qmethod =
"double")

write.table(suma_sum1,paste(resultadosCell,"/Datos_por_Taxa_ELC_Data_by_Taxa
_ELC.xls",sep=""), sep = "\t", row.names = FALSE, col.names=TRUE, qmethod =
"double")
  ##########COMPLEMENTARIEDAD##############################
  ########################################################
  #Función Rebelo modificada
  nspecies <- nrow(tablafin)
  nsites <- ncol(tablafin)
  res <- matrix(ncol=2, nrow=nsites)
  for (i in 1:nsites) {
    sitesppcount <- colSums(tablafin)
    nsp <- max(sitesppcount)
    if (nsp == 0) {break}
    selsite <- which(sitesppcount == nsp)[1]
    selsite2 <- names(selsite)
    res[i,1] <- selsite2
    res[i,2] <- nsp
    delspp <- as.vector(which(tablafin[,selsite]==1))
    tablafin[delspp,] <- 0
```

```
  }
  if(niveltax=="genus"){
    colnames(res) <- c("Celda_Cell", "nGenero_nGenus")
    if(mapaelcf){
      colnames(res) <- c("Celda_Cell", "nGeneroELC_nGenusELC")
    }
  }
  if(niveltax=="species"){
    colnames(res) <- c("Celda_Cell", "nEspecies_nSpecies")
    if(mapaelcf){
      colnames(res) <- c("Celda_Cell", "nEspeciesELC_nSpeciesELC")
    }
  }
  if(niveltax=="subtaxa"){
    colnames(res) <- c("Celda_Cell", "nSubtaxon_nSubtaxa")
    if(mapaelcf){
      colnames(res) <- c("Celda_Cell", "nSubtaxonELC_nSubtaxaELC")
    }
  }

  #Si es de celdas

write.table(res,paste(resultadosCell,"/Tabla_final_Final_Table_Complementa.txt",se
p=""), sep = "\t", row.names = FALSE, qmethod = "double")

write.table(res,paste(resultadosCell,"/Tabla_final_Final_Table_Complementa.xls",se
p=""), sep = "\t", row.names = FALSE, qmethod = "double")


  #Producción mapa resultado
  res<-data.frame(res)
  selected<-subset(res, !is.na(res$Celda_Cell))
```

```
  selected1<-vector()
  for(i in 1:nrow(selected)){
    selected1[i]<-as.numeric(paste(selected[i,1]))
  }
  selected2<-vector()
  for(i in 1:nrow(selected)){
    selected2[i]<-as.numeric(paste(selected[i,2]))
  }
  selected<-data.frame(cbind(selected1,selected2))
  colnames(selected)[1]<-"CELL_ID"
  colnames(selected)[2]<-"N_Taxa"

  #Transformación raster base a raster resultados
  bbb<-subs(aaa,selected,by=1,which=2,subsWithNA=TRUE)

writeRaster(bbb,filename=paste(resultadosCell,"/Complementa_map.grd",sep=""),ov
erwrite=T,datatype='FLT4S')

writeRaster(bbb,filename=paste(resultadosCell,"/Complementa_map.asc",sep=""),for
mat="ascii",overwrite=T,datatype='FLT4S')

  #Análisis top-celdas
  N.Considered.Cells<-nceldas
  Total.Complemental.Cells<-length(selected[,1])
  Perc.Considered.Cells<-100*(nceldas/Total.Complemental.Cells)
  Selected_CELL_ID<-paste(res[1:nceldas,1])
  Taxa.Covered.Considered.Cells<-sum(as.numeric(paste(res[1:nceldas,2])))
  Total.Taxa.Included<-length(filas)
  Perc.Taxa.Covered<-100*(Taxa.Covered.Considered.Cells/length(filas))
  ccc<-data.frame(Selected_CELL_ID)
  colnames(ccc)[1]<-"CELL_ID"
  suma_sum<-merge(suma_sum,ccc, by="CELL_ID",all.y=TRUE)
```

```
  Total.Pop.Covered<-sum(suma_sum[,2])
  Perc.Pop.Covered<-100*(Total.Pop.Covered/length(puntosorig[,1]))
  Parametros.Parameters<-
c("N.Considered.Cells","Total.Complemental.Cells","Perc.Considered.Cells",

"Selected_CELL_ID","Taxa.Covered.Considered.Cells","Total.Taxa.Included","Perc.
Taxa.Covered","Total.Pop.Covered",
                    "Perc.Pop.Covered")
  Valores.Values<-
c(paste(N.Considered.Cells),paste(Total.Complemental.Cells),paste(Perc.Considere
d.Cells),
                paste(Selected_CELL_ID,collapse="
"),paste(Taxa.Covered.Considered.Cells),paste(Total.Taxa.Included),
                paste(Perc.Taxa.Covered),paste(Total.Pop.Covered),
                paste(Perc.Pop.Covered))
  stat.top.celdas<-data.frame(cbind(Parametros.Parameters,Valores.Values))

write.table(stat.top.celdas,paste(resultadosCell,"/Tabla_Estadisticas_Stats_Table_C
omplementa.txt",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")

write.table(stat.top.celdas,paste(resultadosCell,"/Tabla_Estadisticas_Stats_Table_C
omplementa.xls",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")
  tabla_especies<-puntosorigshp@data
  cellvector<-data.frame(as.numeric(paste(res[1:nceldas,1])))
  colnames(cellvector)[1]<-"cellvalue"
  sp_corte<-merge(tabla_especies,cellvector,by="cellvalue",all.y=TRUE)

write.table(sp_corte,paste(resultadosCell,"/Tabla_Pob_en_Top_Celdas_Table_Pop_
in_Top_Cells.txt",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")

write.table(sp_corte,paste(resultadosCell,"/Tabla_Pob_en_Top_Celdas_Table_Pop_
in_Top_Cells.xls",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")
```

```
}

#####################################################################
#####################################################################
#Análisis por Areas de la WDPA
#####################################################################
if(areas){
   #puntosorig<-puntosorig[,1:10]

   ###############################################################
   #####Por áreas de la WDPA####################
  if(WDPA){
   #creación directorio para análisis de celdas
   setwd(paste(resultados))
   dir.create(as.vector(paste("AnalisisWDPA_WDPAAnalysis")))
   resultadosWDPA<-paste(resultados,"/AnalisisWDPA_WDPAAnalysis",sep="")
   #Carga de mapa WDPA
   setwd(paste(ruta))
   load("lista.paises.RData")
   pais<-subset(Paises,Denomina==paste(pais))
   pais<-paste(pais[1,1])
   setwd(paste(ruta,"/wdpa",sep=""))
   load(paste(pais,".RData",sep=""))
   #Creación de puntos
   puntos<-SpatialPoints(puntosorig[,c(6,5)])
   #extracción y conformación tabla
   wdpa<-over(puntos,aaa)
   tablatotal<-cbind(puntosorig,wdpa)

write.table(tablatotal,paste(resultadosWDPA,"/Tabla_Pob_en_fuera_WDPA_Table_
Pop_in_out_WDPA.txt",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")
```

```
write.table(tablatotal,paste(resultadosWDPA,"/Tabla_Pob_en_fuera_WDPA_Table_
Pop_in_out_WDPA.xls",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")
    if(coveran){
      setwd(paste(resultadosWDPA))
      dir.create(as.vector(paste("CoverageAnalysis")))
      resultadosCOVERAN<-
paste(resultados,"/AnalisisWDPA_WDPAAnalysis/CoverageAnalysis",sep="")
      tablain<-subset(tablatotal,!is.na(wdpaid))
      tablaout<-subset(tablatotal,is.na(wdpaid))
      areasWDPA<-data.frame(table(tablain$wdpaid))
      colnames(areasWDPA)[1]<-"wdpaid"
      colnames(areasWDPA)[2]<-"N_Pops"
      N_Diff_Taxa<-vector()
      for(i in 1:length(areasWDPA[,1])){
        ttt<-subset(tablain,wdpaid==areasWDPA[i,1])
        N_Diff_Taxa[i]<-length(unique(ttt$CHAIN))
      }
      areasWDPA<-cbind(areasWDPA,N_Diff_Taxa)

write.table(areasWDPA,paste(resultadosCOVERAN,"/Tabla_AreasWDPA_Cubriend
o_AreasWDPA_Covering_Table.txt",sep=""), sep = "\t", row.names = FALSE,
col.names=TRUE, qmethod = "double")

write.table(areasWDPA,paste(resultadosCOVERAN,"/Tabla_AreasWDPA_Cubriend
o_AreasWDPA_Covering_Table.xls",sep=""), sep = "\t", row.names = FALSE,
col.names=TRUE, qmethod = "double")
      eee<-aaa@data
      eee<-match(areasWDPA$wdpaid,eee$wdpaid)
      ttt<-aaa[eee,]
      areasWDPA<-areasWDPA[,-1]
      rownames(areasWDPA)<-rownames(ttt@data)
```

```
    ttt<-spCbind(ttt,areasWDPA)
    writePolyShape(ttt,paste(resultadosCOVERAN,"/CoverWDPAmap",sep=""))
    taxain<-data.frame(table(tablain$CHAIN))
    colnames(taxain)[1]<-"Taxa"
    colnames(taxain)[2]<-"Pops_Conserved"
    taxatotal<-data.frame(table(tablatotal$CHAIN))
    colnames(taxatotal)[1]<-"Taxa_TaxaELC"
    colnames(taxatotal)[2]<-"Total_N_Pops"
    taxa<-cbind(taxatotal,taxain[,2])
    colnames(taxa)[3]<-"Pops_in_WDPA"
    Perc_Pops_in<-100*(taxa$Pops_in_WDPA/taxa$Total_N_Pops)
    taxa<-cbind(taxa,Perc_Pops_in)

write.table(taxa,paste(resultadosCOVERAN,"/Tabla_Taxa_Cubiertos_Table_Taxa_Covered.txt",sep=""), sep = "\t", row.names = FALSE, col.names=TRUE, qmethod = "double")

write.table(taxa,paste(resultadosCOVERAN,"/Tabla_Taxa_Cubiertos_Table_Taxa_Covered.xls",sep=""), sep = "\t", row.names = FALSE, col.names=TRUE, qmethod = "double")
    #TablaStats
    Pops_Covered<-sum(areasWDPA$N_Pops)
    Perc_Pops_Covered<-100*(Pops_Covered/nrow(puntosorig))
    ntaxain<-length(unique(tablain$CHAIN))
    ntaxatot<-length(unique(tablatotal$CHAIN))
    Taxa_Covered<-ntaxain
    Perc_Taxa_Covered<-100*(ntaxain/ntaxatot)
    N_WDPA_Cov_Pops<-length(unique(tablain$wdpaid))
    Perc_WDPA_Cov<-100*(N_WDPA_Cov_Pops/nrow(aaa@data))
    Parametros.Parameters<-c("Pops_Covered","Perc_Pops_Covered",
                             "Taxa_Covered","Perc_Taxa_Covered",
                             "N_WDPA_Cov_Pops","Perc_WDPA_Cov")
```

```
    Valores.Values<-c(paste(Pops_Covered),paste(Perc_Pops_Covered),
                      paste(Taxa_Covered),paste(Perc_Taxa_Covered),
                      paste(N_WDPA_Cov_Pops),paste(Perc_WDPA_Cov))
    stat.cov.areas<-data.frame(cbind(Parametros.Parameters,Valores.Values))

write.table(stat.cov.areas,paste(resultadosCOVERAN,"/Tabla_Estadisticas_Cobertura_Stats_Table_Coverage.txt",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")

write.table(stat.cov.areas,paste(resultadosCOVERAN,"/Tabla_Estadisticas_Cobertura_Stats_Table_Coverage.xls",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")
    setwd(paste(ruta))
  }
  puntosorig<-tablatotal[,1:11]
  puntosorig1<-subset(puntosorig,!is.na(wdpaid))

  #Arreglo tabla para complementariedad
  ###Armado de tabla para Rebelo
  #lista de valores de celda mapa molde
  columnas<-unique(puntosorig1$wdpaid)
  #lista genus-especies-subsp-elc
  filas<-unique(puntosorig1$CHAIN)
  #Armazón
  tablafin<-matrix(data=0,nrow=length(filas),ncol=length(columnas))
  colnames(tablafin)<-columnas
  rownames(tablafin)<-filas
  for(i in 1:length(filas)){
    tabla1<-subset(puntosorig1,puntosorig1$CHAIN==paste(filas[i]))
    tabla1<-unique(tabla1$wdpaid)
    for (j in 1:length(columnas)){
      if(any(tabla1==colnames(tablafin)[j])){
```

```
        tablafin[i,j]<-1
       }
      }
    }
    #Se salva la tabla
    tablafin2<-cbind(as.character(filas),tablafin)
    colnames(tablafin2)[1]<-"Genus_Sp_Subtaxa_ELC"
    write.table(tablafin2,paste(resultadosWDPA,"/Tabla_Table_Base.txt",sep=""),   sep
= "\t", row.names = FALSE, col.names=TRUE, qmethod = "double")
    write.table(tablafin2,paste(resultadosWDPA,"/Tabla_Table_Base.xls",sep=""),  sep
= "\t", row.names = FALSE, col.names=TRUE, qmethod = "double")

    ##########COMPLEMENTARIEDAD##############################
    ########################################################
    #Función Rebelo modificada
    nspecies <- nrow(tablafin)
    nsites <- ncol(tablafin)
    res <- matrix(ncol=2, nrow=nsites)
    for (i in 1:nsites) {
      sitesppcount <- colSums(tablafin)
      nsp <- max(sitesppcount)
      if (nsp == 0) {break}
      selsite <- which(sitesppcount == nsp)[1]
      selsite2 <- names(selsite)
      res[i,1] <- selsite2
      res[i,2] <- nsp
      delspp <- as.vector(which(tablafin[,selsite]==1))
      tablafin[delspp,] <- 0
    }
    if(niveltax=="genus"){
      colnames(res) <- c("wdpaid", "nGenero_nGenus")
      if(mapaelcf){
```

```
      colnames(res) <- c("wdpaid", "nGeneroELC_nGenusELC")
    }
  }
  if(niveltax=="species"){
    colnames(res) <- c("wdpaid", "nEspecies_nSpecies")
    if(mapaelcf){
      colnames(res) <- c("wdpaid", "nEspeciesELC_nSpeciesELC")
    }
  }
  if(niveltax=="subtaxa"){
    colnames(res) <- c("wdpaid", "nSubtaxon_nSubtaxa")
    if(mapaelcf){
      colnames(res) <- c("wdpaid", "nSubtaxonELC_nSubtaxaELC")
    }
  }

  #Si es de Areas

write.table(res,paste(resultadosWDPA,"/Tabla_final_Final_Table_Complementa.txt",
sep=""), sep = "\t", row.names = FALSE, qmethod = "double")

write.table(res,paste(resultadosWDPA,"/Tabla_final_Final_Table_Complementa.xls",
sep=""), sep = "\t", row.names = FALSE, qmethod = "double")

  #Producción mapa resultado
  res<-data.frame(res)
  selected<-subset(res, !is.na(res$wdpaid))
  selected1<-vector()
  for(i in 1:nrow(selected)){
    selected1[i]<-as.numeric(paste(selected[i,1]))
  }
  selected2<-vector()
```

```
    for(i in 1:nrow(selected)){
      selected2[i]<-as.numeric(paste(selected[i,2]))
    }
    selected<-data.frame(cbind(selected1,selected2))
    colnames(selected)[1]<-"wdpaid"
    colnames(selected)[2]<-"N_Taxa"
    selected2<-aaa$wdpaid
    indice<-match(selected$wdpaid,selected2)
    bbb<-aaa[indice,]
    N_Taxa<-selected$N_Taxa
    bbb<-spCbind(bbb,N_Taxa)
    #exportar mapas y puntos
    puntos<-SpatialPointsDataFrame(tablatotal[,c(6,5)],tablatotal)

writePointsShape(puntos,paste(resultadosWDPA,"/final_analyzed_points",sep=""))
    writePolyShape(aaa,paste(resultadosWDPA,"/TotalWDPAmap",sep=""))

writePolyShape(bbb,paste(resultadosWDPA,"/ComplementaryWDPAmap",sep=""))

    #Análisis top-áreas
    N.Considered.WDPA<-nareas
    Total.Complemental.WDPA<-length(selected[,1])
    Perc.Considered.WDPA<-100*(nareas/Total.Complemental.WDPA)
    Selected_WDPA_ID<-paste(res[1:nareas,1])
    Taxa.Covered.Considered.WDPA<-sum(as.numeric(paste(res[1:nareas,2])))
    Total.Taxa.Included<-length(filas)
    Perc.Taxa.Covered<-100*(Taxa.Covered.Considered.WDPA/length(filas))
    ccc<-data.frame(Selected_WDPA_ID)
    colnames(ccc)[1]<-"wdpaid"
    suma_sum<-merge(tablatotal,ccc, by="wdpaid",all.y=TRUE)
    Total.Pop.Covered<-length(suma_sum[,1])
    Perc.Pop.Covered<-100*(Total.Pop.Covered/length(tablatotal[,1]))
```

```
   Parametros.Parameters<-
c("N.Considered.WDPA","Total.Complemental.WDPA","Perc.Considered.WDPA",

"Selected_WDPA_ID","Taxa.Covered.Considered.WDPA","Total.Taxa.Included","Pe
rc.Taxa.Covered","Total.Pop.Covered",
                        "Perc.Pop.Covered")
   Valores.Values<-
c(paste(N.Considered.WDPA),paste(Total.Complemental.WDPA),paste(Perc.Consid
ered.WDPA),
                  paste(Selected_WDPA_ID,collapse=",
"),paste(Taxa.Covered.Considered.WDPA),paste(Total.Taxa.Included),
                  paste(Perc.Taxa.Covered),paste(Total.Pop.Covered),
                  paste(Perc.Pop.Covered))
   stat.top.areas<-data.frame(cbind(Parametros.Parameters,Valores.Values))

write.table(stat.top.areas,paste(resultadosWDPA,"/Tabla_Estadisticas_Stats_Table_
Complementa.txt",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")

write.table(stat.top.areas,paste(resultadosWDPA,"/Tabla_Estadisticas_Stats_Table_
Complementa.xls",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")

write.table(suma_sum,paste(resultadosWDPA,"/Tabla_Pob_en_Top_WDPA_Table_
Pop_in_Top_WDPA.txt",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")

write.table(suma_sum,paste(resultadosWDPA,"/Tabla_Pob_en_Top_WDPA_Table_
Pop_in_Top_WDPA.xls",sep=""), sep = "\t", row.names = FALSE, qmethod =
"double")
  }
}

#########################################################################
#########################################################################
```

```
#####Por áreas protegidas propios#################################
if(areas){
  #puntosorig<-puntosorig[,1:10]
  if(propio){
    #Directorio
    setwd(paste(resultados))
    #creación directorio para análisis de áreas propias
    dir.create(as.vector(paste("AnalisisAreasProt_ProtectedAreasAnalysis")))
    resultadosWDPA<-
paste(resultados,"/AnalisisAreasProt_ProtectedAreasAnalysis",sep="")
    setwd(paste(ruta))
    #ingreso área protegida
    areasprot<-readShapePoly(paste("wdpa/",nombre,".shp",sep=""))
    #Puntos
    puntos<-SpatialPoints(puntosorig[,c(6,5)])
    #extracción y conformación tabla
    wdpa<-over(puntos,areasprot)
    tablatotal<-cbind(puntosorig,wdpa)

write.table(tablatotal,paste(resultadosWDPA,"/Tabla_Pob_en_fuera_AreasProt_Table_Pop_in_out_ProtAreas.txt",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")

write.table(tablatotal,paste(resultadosWDPA,"/Tabla_Pob_en_fuera_AreasProt_Table_Pop_in_out_ProtAreas.xls",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")
    if(coveran){
      setwd(paste(resultadosWDPA))
      dir.create(as.vector(paste("CoverageAnalysis")))
      resultadosCOVERAN<-
paste(resultados,"/AnalisisAreasProt_ProtectedAreasAnalysis/CoverageAnalysis",sep="")
```

```
ind1<-match(campo,colnames(tablatotal))
tablain<-subset(tablatotal,!is.na(tablatotal[,ind1]))
tablaout<-subset(tablatotal,is.na(tablatotal[,ind1]))
ind2<-match(campo,colnames(tablain))
areasWDPA<-data.frame(table(tablain[,ind2]))
colnames(areasWDPA)[1]<-campo
colnames(areasWDPA)[2]<-"N_Pops"
N_Diff_Taxa<-vector()
for(i in 1:length(areasWDPA[,1])){
  ttt<-subset(tablain,tablain[,ind2]==areasWDPA[i,1])
  N_Diff_Taxa[i]<-length(unique(ttt$CHAIN))
}
areasWDPA<-cbind(areasWDPA,N_Diff_Taxa)

write.table(areasWDPA,paste(resultadosCOVERAN,"/Tabla_AreasProt_Cubriendo_
ProtAreas_Covering_Table.txt",sep=""), sep = "\t", row.names = FALSE,
col.names=TRUE, qmethod = "double")

write.table(areasWDPA,paste(resultadosCOVERAN,"/Tabla_AreasProt_Cubriendo_
ProtAreas_Covering_Table.xls",sep=""), sep = "\t", row.names = FALSE,
col.names=TRUE, qmethod = "double")
eee<-areasprot@data
ind3<-match(campo,colnames(eee))
eee<-match(areasWDPA[,1],eee[,ind3])
ttt<-areasprot[eee,]
areasWDPA<-areasWDPA[,-1]
rownames(areasWDPA)<-rownames(ttt@data)
ttt<-spCbind(ttt,areasWDPA)
writePolyShape(ttt,paste(resultadosCOVERAN,"/CoverAREASmap",sep=""))
taxain<-data.frame(table(tablain$CHAIN))
colnames(taxain)[1]<-"Taxa"
colnames(taxain)[2]<-"Pops_Conserved"
```

```
    taxatotal<-data.frame(table(tablatotal$CHAIN))
    colnames(taxatotal)[1]<-"Taxa_TaxaELC"
    colnames(taxatotal)[2]<-"Total_N_Pops"
    taxa<-cbind(taxatotal,taxain[,2])
    colnames(taxa)[3]<-"Pops_in_AREAS"
    Perc_Pops_in<-100*(taxa$Pops_in_AREAS/taxa$Total_N_Pops)
    taxa<-cbind(taxa,Perc_Pops_in)
write.table(taxa,paste(resultadosCOVERAN,"/Tabla_Taxa_Cubiertos_Table_Taxa_Covered.txt",sep=""), sep = "\t", row.names = FALSE, col.names=TRUE, qmethod = "double")
write.table(taxa,paste(resultadosCOVERAN,"/Tabla_Taxa_Cubiertos_Table_Taxa_Covered.xls",sep=""), sep = "\t", row.names = FALSE, col.names=TRUE, qmethod = "double")
    #TablaStats
    Pops_Covered<-sum(areasWDPA$N_Pops)
    Perc_Pops_Covered<-100*(Pops_Covered/nrow(puntosorig))
    ntaxain<-length(unique(tablain$CHAIN))
    ntaxatot<-length(unique(tablatotal$CHAIN))
    Taxa_Covered<-ntaxain
    Perc_Taxa_Covered<-100*(ntaxain/ntaxatot)
    N_Areas_Cov_Pops<-length(unique(tablain[,ind2]))
    Perc_Areas_Cov<-100*(N_Areas_Cov_Pops/nrow(areasprot@data))
    Parametros.Parameters<-c("Pops_Covered","Perc_Pops_Covered",
                             "Taxa_Covered","Perc_Taxa_Covered",
                             "N_Areas_Cov_Pops","Perc_Areas_Cov")
    Valores.Values<-c(paste(Pops_Covered),paste(Perc_Pops_Covered),
                      paste(Taxa_Covered),paste(Perc_Taxa_Covered),
                      paste(N_Areas_Cov_Pops),paste(Perc_Areas_Cov))
    stat.cov.areas<-data.frame(cbind(Parametros.Parameters,Valores.Values))
write.table(stat.cov.areas,paste(resultadosCOVERAN,"/Tabla_Estadisticas_Cobertura_Stats_Table_Coverage.txt",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")
```

```
write.table(stat.cov.areas,paste(resultadosCOVERAN,"/Tabla_Estadisticas_Cobertura_Stats_Table_Coverage.xls",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")
    setwd(paste(ruta))
  }
  campo1<-tablatotal[,campo]
  puntosorig<-cbind(puntosorig,campo1)
  colnames(puntosorig)[ncol(puntosorig)]<-campo
  puntosorig1<-subset(puntosorig,!is.na(puntosorig[,ncol(puntosorig)]))
  #Arreglo tabla para complementariedad
  ###Armado de tabla para Rebelo
  #lista de valores de celda mapa molde
  columnas<-unique(puntosorig1[,ncol(puntosorig1)])
  #lista genus-especies-subsp-elc
  filas<-unique(puntosorig1$CHAIN)
  #Armazón
  tablafin<-matrix(data=0,nrow=length(filas),ncol=length(columnas))
  colnames(tablafin)<-columnas
  rownames(tablafin)<-filas
  for(i in 1:length(filas)){
   tabla1<-subset(puntosorig1,puntosorig1$CHAIN==paste(filas[i]))
   tabla1<-unique(tabla1[,ncol(tabla1)])
   for (j in 1:length(columnas)){
    if(any(tabla1==colnames(tablafin)[j])){
     tablafin[i,j]<-1
    }
   }
  }
  #Se salva la tabla
  tablafin2<-cbind(as.character(filas),tablafin)
  colnames(tablafin2)[1]<-"Genus_Sp_Subtaxa_ELC"
```

```
    write.table(tablafin2,paste(resultadosWDPA,"/Tabla_Table_Base.txt",sep=""),   sep
= "\t", row.names = FALSE, col.names=TRUE, qmethod = "double")
    write.table(tablafin2,paste(resultadosWDPA,"/Tabla_Table_Base.xls",sep=""),  sep
= "\t", row.names = FALSE, col.names=TRUE, qmethod = "double")
    #########COMPLEMENTARIEDAD##############################
    ########################################################
    #Función Rebelo modificada
    nspecies <- nrow(tablafin)
    nsites <- ncol(tablafin)
    res <- matrix(ncol=2, nrow=nsites)
    for (i in 1:nsites) {
      sitesppcount <- colSums(tablafin)
      nsp <- max(sitesppcount)
      if (nsp == 0) {break}
      selsite <- which(sitesppcount == nsp)[1]
      selsite2 <- names(selsite)
      res[i,1] <- selsite2
      res[i,2] <- nsp
      delspp <- as.vector(which(tablafin[,selsite]==1))
      tablafin[delspp,] <- 0
    }
    if(niveltax=="genus"){
      colnames(res) <- c("areaID", "nGenero_nGenus")
      if(mapaelcf){
        colnames(res) <- c("areaID", "nGeneroELC_nGenusELC")
      }
    }
    if(niveltax=="species"){
      colnames(res) <- c("areaID", "nEspecies_nSpecies")
      if(mapaelcf){
        colnames(res) <- c("areaID", "nEspeciesELC_nSpeciesELC")
      }
```

```
    }
    if(niveltax=="subtaxa"){
      colnames(res) <- c("areaID", "nSubtaxon_nSubtaxa")
      if(mapaelcf){
        colnames(res) <- c("areaID", "nSubtaxonELC_nSubtaxaELC")
      }
    }

    #Si es de Areas

write.table(res,paste(resultadosWDPA,"/Tabla_final_Final_Table_Complementa.txt",
sep=""), sep = "\t", row.names = FALSE, qmethod = "double")

write.table(res,paste(resultadosWDPA,"/Tabla_final_Final_Table_Complementa.xls",
sep=""), sep = "\t", row.names = FALSE, qmethod = "double")

    #Producción mapa resultado
    res<-data.frame(res)
    selected<-subset(res, !is.na(res$areaID))
    colnames(selected)[1]<-"areaID"
    colnames(selected)[2]<-"N_Taxa"
    selected2<-areasprot@data
    selected2<-paste(selected2[,campo])
    indice<-match(selected$areaID,selected2)
    bbb<-areasprot[indice,]
    N_Taxa<-as.numeric(paste(selected$N_Taxa))
    bbb<-spCbind(bbb,N_Taxa)
    #exportar mapas y puntos
    puntos<-SpatialPointsDataFrame(tablatotal[,c(6,5)],tablatotal)

writePointsShape(puntos,paste(resultadosWDPA,"/final_analyzed_points",sep=""))
    writePolyShape(bbb,paste(resultadosWDPA,"/ComplementAreas",sep=""))
```

```
    writePolyShape(aaa,paste(resultadosWDPA,"/TotalWDPA_Areas",sep=""))
    #Análisis top-áreas
    N.Considered.Areas<-nareas
    Total.Complemental.Areas<-length(selected[,1])
    Perc.Considered.Areas<-100*(nareas/Total.Complemental.Areas)
    Selected_Areas_ID<-paste(res[1:nareas,1])
    Taxa.Covered.Considered.Areas<-sum(as.numeric(paste(res[1:nareas,2])))
    Total.Taxa.Included<-length(filas)
    Perc.Taxa.Covered<-100*(Taxa.Covered.Considered.Areas/length(filas))
    ccc<-data.frame(Selected_Areas_ID)
    colnames(ccc)[1]<-campo
    suma_sum<-merge(tablatotal,ccc, by=campo,all.y=TRUE)
    Total.Pop.Covered<-length(suma_sum[,1])
    Perc.Pop.Covered<-100*(Total.Pop.Covered/length(tablatotal[,1]))
    Parametros.Parameters<-
c("N.Considered.Areas","Total.Complemental.Areas","Perc.Considered.Areas",

"Selected_Areas_ID","Taxa.Covered.Considered.Areas","Total.Taxa.Included","Perc
.Taxa.Covered","Total.Pop.Covered",
                        "Perc.Pop.Covered")
    Valores.Values<-
c(paste(N.Considered.Areas),paste(Total.Complemental.Areas),paste(Perc.Consider
ed.Areas),
                    paste(Selected_Areas_ID,collapse=",
"),paste(Taxa.Covered.Considered.Areas),paste(Total.Taxa.Included),
                    paste(Perc.Taxa.Covered),paste(Total.Pop.Covered),
                    paste(Perc.Pop.Covered))
    stat.top.areas<-data.frame(cbind(Parametros.Parameters,Valores.Values))

write.table(stat.top.areas,paste(resultadosWDPA,"/Tabla_Estadisticas_Stats_Table_
Complementa.txt",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")
```

```
write.table(stat.top.areas,paste(resultadosWDPA,"/Tabla_Estadisticas_Stats_Table_
Complementa.xls",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")
write.table(suma_sum,paste(resultadosWDPA,"/Tabla_Pob_en_Top_Areas_Table_P
op_in_Top_Areas.txt",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")

write.table(suma_sum,paste(resultadosWDPA,"/Tabla_Pob_en_Top_Areas_Table_P
op_in_Top_Areas.xls",sep=""), sep = "\t", row.names = FALSE, qmethod = "double")
  }
}
writePolyShape(aaa,paste(resultadosWDPA,"/ComplementAreas",sep=""))
setwd("C:/")
```

Supplementary material 2, Red List assessment.

Species	**Global Red List Status**
1. *Avena fatua* - L.	LC - Least Concern, (IUCN version 3.1)
2. Avena hybrida Peterm.	DD - Data Deficient, (IUCN version 3.1)
3. *Avena sterilis* - L.	LC - Least Concern, (IUCN version 3.1)
4. *Cicer bijugum* - Rech.f.	EN - Endangered, b2ab(iii) (IUCN version 3.1)
5. *Cicer echinospermum* - P.H. Davis	LC - Least Concern, (IUCN version 3.1)
6. *Cicer judaicum* - Boiss.	DD - Data Deficient, (IUCN version 3.1)
7. *Cicer pinnatifidum* - Jaub. & Spach	DD - Data Deficient, (IUCN version 3.1)
8. *Cicer reticulatum* - Ladiz.	Near Threatened (NT) (IUCN version 3.1)
9. Hordeum brevisubulatum (Trin.) Link	LC - Least Concern, (IUCN version 3.1)
10. *Hordeum bulbosum* - L.	LC - Least Concern, (IUCN version 3.1)
11. *Medicago lanigera* - C.Winkl. & B. Fedtsch.	Near Threatened (NT) (IUCN version 3.1)
12. *Medicago arabica* - (L.) Huds.	LC - Least Concern, (IUCN version 3.1)
13. Medicago archiducis-nicolai Širj	Near Threatened (NT), (IUCN version 3.1)
14. *Medicago arenicola* - (Hub.-Mor.) E.Small	DD - Data Deficient (IUCN version 3.1)
15. *Medicago biflora* - (Griseb.) E.Small	LC - Least Concern, (IUCN version 3.1)

16. *Medicago bonarotiana* - Arcang.	LC - Least Concern, (IUCN version 3.1)
17. Medicago brachycarpa - Fisch. Ex M. Bieb.	LC - Least Concern, (IUCN version 3.1)
18. *Medicago cancellata* - M. Bieb.	Near Threatened (NT), (IUCN version 3.1)
19. *Medicago carica* - (Hub.-Mor.) E. Small	Near Threatened (NT), (IUCN version 3.1)
20. *Medicago carstiensis* - Wulfen	LC - Least Concern, (IUCN version 3.1)
21. *Medicago ciliaris* - (L.) All.	LC - Least Concern, (IUCN version 3.1)
22. *Medicago coronata* - (L.) Bar tal.	LC - Least Concern, (IUCN version 3.1)
23. *Medicago crassipes* - (Boiss.) E.Small	EN - Endangered, b2ab(iii) (IUCN version 3.1)
24. *Medicago cretacea* - M. Bieb.	EN - Endangered, b2b(iii)c(iv) (IUCN version 3.1)
25. *Medicago daghestanica* - Rupr.	DD - Data Deficient, (IUCN version 3.1)
26. Medicago disciformis - DC.	LC - Least Concern, (IUCN version 3.1)
27. *Medicago edgeworthii* - Širj.	Near Threatened (NT), (IUCN version 3.1)
28. *Medicago fischeriana* - (Ser.) Trautv.	LC - Least Concern, (IUCN version 3.1)
29. *Medicago granadensis* - Willd.	DD - Data Deficient, B2a (IUCN version 3.1)

30. *Medicago halophila* - (Boiss.) E.Small	CR - Critically Endangered, b2ab(i,iii) (IUCN version 3.1)
31. *Medicago heldreichii* - E.Small	Near Threatened (NT). (IUCN version 3.1)
32. *Medicago huberi* - E.Small	Near Threatened (NT). (IUCN version 3.1)
33. *Medicago hybrida*- (Pourr.) Trautv.	LC - Least Concern, (IUCN version 3.1)
34. *Medicago hypogaea* - E. Small	Near Threatened (NT), (IUCN version 3.1)
35. *Medicago intertexta* - (L.) Mill.	LC - Least Concern, (IUCN version 3.1)
36. *Medicago isthmocarpa* - (Boiss. & Balansa) E.Small	Near Threatened (NT) (IUCN version 3.1)
37. *Medicago italica* - (mill.) Fiori	LC - Least Concern, (IUCN version 3.1)
38. *Medicago laciniata*- (L.) Mill.	LC - Least Concern, (IUCN version 3.1)
39. *Medicago laxispira* - Heyn	Near Threatened (NT) (IUCN version 3.1)
40. Medicago littoralis var. Littoralis - Rohde ex Loisel.	DD - Data Deficient, (IUCN version 3.1)
41. *Medicago marina* - L.	LC - Least Concern, (IUCN version 3.1)
42. *Medicago medicaginoides* - (Retz.) E. Small	LC - Least Concern, B2a (IUCN version 3.1)
43. *Medicago monantha*- (C.A.Mey.) Trautv.	LC - Least Concern (IUCN version 3.1)
44. Medicago monspeliaca - (L.) Trautv.	LC - Least Concern (IUCN version 3.1)

45. *Medicago muricoleptis*- Tineo	DD - Data Deficient, (IUCN version 3.1)
46. *Medicago noeana* - Boiss.	Near Threatened (NT) (IUCN version 3.1)
47. *Medicago orbicularis* - (L.) Bartal.	LC - Least Concern, (IUCN version 3.1)
48. *Medicago orthoceras* - Trautv.	Near Threatened (NT) (IUCN version 3.1)
49. *Medicago ovalis* - Urb.	Near Threatened (NT) (IUCN version 3.1)
50. *Medicago pamphylica* - (Hub.-Mor. & Sirj.) E.Small	Near Threatened (NT). (IUCN version 3.1)
51. *Medicago papillosa* - Boiss.	Near Threatened (NT), b2b(v) (IUCN version 3.1)
52. *Medicago persica* - (Boiss.) E.Small	Near Threatened (NT), (IUCN version 3.1)
53. *Medicago phrygia* - (Boiss.) E. Small	DD - Data Deficient, (IUCN version 3.1)
54. *Medicago plicata* - (Boiss.) Širj.	DD - Data Deficient, (IUCN version 3.1)
55. *Medicago polyceratia* - (L.) Trautv.	LC - Least Concern, (IUCN version 3.1)
56. *Medicago polymorpha* L	LC - Least Concern, (IUCN version 3.1)
57. *Medicago popovii* - Širj.	Near Threatened (NT). (IUCN version 3.1)
58. *Medicago praecox* - DC.	LC - Least Concern, (IUCN version 3.1)
59. Medicago prostrata - Jacq.	LC - Least Concern, (IUCN version 3.1)
60. *Medicago radiata* - L.	LC - Least Concern, (IUCN version 3.1)
61. *Medicago retrorsa* - (Boiss.) E.Small	DD - Data Deficient, (IUCN version 3.1)

62. *Medicago rhodopea* - Velen.	DD - Data Deficient, (IUCN version 3.1)
63. *Medicago rhytidiocarpa* - (Boiss. & Balansa) E.Small	Near Threatened (NT), B2a (IUCN version 3.1)
64. *Medicago rigida* - (Boiss. & Balansa) E.Small	Near Threatened (NT), B2a (IUCN version 3.1)
65. *Medicago rigiduloides* - E.Small	LC - Least Concern, (IUCN version 3.1)
66. *Medicago rostrata* - (Boiss. & Balansa) E.Small	Near Threatened (NT), (IUCN version 3.1)
67. *Medicago rupestris* - M. Bieb.	Near Threatened (NT), (IUCN version 3.1)
68. *Medicago ruthenica* - (L.) Trautv.	Near Threatened (NT), (IUCN version 3.1)
69. *Medicago sauvagei* Negre	Near Threatened (NT), (IUCN version 3.1)
70. *Medicago shepardii* - Post. Ex Boiss.	Near Threatened (NT), (IUCN version 3.1)
71. *Medicago sinskiae* - Uljanova	DD - Data Deficient, (IUCN version 3.1)
72. Medicago suffruticosa - Ramond ex DC.	LC - Least Concern, (IUCN version 3.1)
73. *Medicago syriaca* - E.Small	DD - Data Deficient, (IUCN version 3.1)
74. *Triticum aestivum L. Subsp. Tibeticum* J. Z. Shao.	DD - Data Deficient, (IUCN version 3.1)
75. Triticum monococcum - L.	LC - Least Concern, (IUCN version 3.1)

76. *Triticum monococcum* - L. Subsp*. Monococcum*	LC - Least Concern, (IUCN version 3.1)
77. *Triticum monococcum L. Subsp. Aegilopoides (Link) Thell.*	LC - Least Concern, (IUCN version 3.1)
78. Triticum timopheevii (Zhuk.) Zhuk.	LC - Least Concern, (IUCN version 3.1)
79. *Triticum timopheevii (Zhuk.) Zhuk. Subsp. Armeniacum (Jakubz.) Slageren*	DD - Data Deficient, (IUCN version 3.1)
80. *Triticum timopheevii (Zhuk.) Zhuk. Subsp. Timopheevii*	DD - Data Deficient, (IUCN version 3.1)
81. Triticum turgidum	LC - Least Concern, (IUCN version 3.1)
82. Triticum turgidum L. Subsp. Carthlicum (Nevski) A. Love & D. Love	LC - Least Concern, (IUCN version 3.1)
83. Triticum turgidum L. Subsp. Dicoccoides (Korn. Ex Asch. & Graebn.) Thell. - L.	LC - Least Concern, (IUCN version 3.1)
84. Triticum turgidum L. Subsp. Paleocolchicum Á. Löve & D. Löve.	LC - Least Concern, (IUCN version 3.1)
85. Triticum turgidum L. Subsp. Polonicum (L.) Thell.	LC - Least Concern, (IUCN version 3.1)
86. Triticum turgidum L. Subsp. Turanicum (Jakubz.) A. Love & D. Love.	LC - Least Concern, (IUCN version 3.1)
87. Triticum urartu	DD - Data Deficient (IUCN version 3.1)
88. *Triticum urartu* - Tumanian ex Gandilyan	LC - Least Concern, (IUCN version 3.1)